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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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                    // Cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
// Cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
// Cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
// Cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
// Cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
// Cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
// Cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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// Cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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14.9	14.9	15.0	15.0	15.0	15.0	15.0	15.1	15.4	15.4	15.4	99.8	99.8	99.8	Query
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Sequence 3, Appli	Sequence 3, Appli	Sequence 51, Appl	Sequence 688, App	Sequence 1102, Ap	Sequence 883, App	Seguence 1041, Ap	Sequence 12, Appl	Sequence 12, Appl	Sequence 61, Appl	Description				

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APPLICANT: Rosen et al.
TITLE OP INVENTION: 90 Human Secreted Proteins; FILE REFERENCE: PZ013P1
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                                                                                                                                                                                          Matches 867;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. SEQ ID NO 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/774,639
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
PRIOR FILING DATE: BARLIER FILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 371
                                                                                                                                                                                                                                                                                                                                 NAME/KEY: SITE
LOCATION: (831)
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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61 GGTCTCGAACTCCTGACCTCGTGATCCGCCCGCCTCCGCCTCCCAAAGTGCTGGGATTAC 120
                              61 GGTCTCGAACTCCTGACCTCGTGATCCCGCCCGCCCTCCGGCCTCCCAAAGTGCTGGGGATTAC 120
                                                                                              1 TCGAGTTTTTTTTTTTTTTTTTTTTAAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGAT 60
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PRIOR APPLICATION NUMBER: 09/744,639
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2001-02-01
PRIOR PRILING DATE: 2001-02-01
PRIOR PRILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: 60/238,291
PRIOR APPLICATION NUMBER: 09/244,112
PRIOR APPLICATION NUMBER: 09/244,112
PRIOR PRILING DATE: 1999-02-04
PRIOR PILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/056,371
PRIOR PRILING DATE: 1997-08-19
                                                                                                                                                                                                                                                                                                                                          US-09-969-730-12
                                                                                                                                                                                                                                                                                     Sequence 12, Application US/09969730 Publication No. US20030054443A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                APPLICANT: Ruben et al.
TITLE OF INVENTION: 90 Human Secreted Proteins
FILS REFERENCE: PZ013P2
                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/969,730 CURRENT FILING DATE: 2001-10-04
APPLICATION NUMBER: 60/056,732
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; FEATURE:
; NAME/KEY: SITE
; LOCATION: (831)
; OTHER INFORMATION: n equ
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; LENGTH: 867
; TYPE: DNA
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PRIOR FILING DATE: 1997-08-05-
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FILING DATE: 1997-08-05
APPLICATION NUMBER: 60/054,809
FILING DATE: 1997-08-05
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FILING DATE: 1997-08-19
APPLICATION NUMBER: 60/
FILING DATE: 1997-08-18
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RESULT 3
US-10-621-363-12
PRIOR APPLICATION NUMBER: 60/238,291
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 09/244,112
PRIOR FILING DATE: 1999-02-04
PRIOR FILING DATE: 1999-02-04
PRIOR FILING DATE: 1999-08-04
PRIOR PLLING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/056,371
PRIOR APPLICATION NUMBER: 60/056,371
PRIOR APPLICATION NUMBER: 60/056,732
PRIOR FILING DATE: 1997-08-19
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/10621363
Publication No. US20040023283A1
GENERAL INFORMATION:
                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/621,363
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/969,730
PRIOR FILING DATE: 2001-10-06
PRIOR APPLICATION NUMBER: 09/774,639
PRIOR FILING DATE: 2001-02-01
PRIOR FILING DATE: 2001-02-01
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ruben et al.
TITLE OF INVENTION: 90 Human Secreted Proteins
FILB REFERENCE: PZ011P2C1
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SEQ ID NO 12
LENGTH: 867
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Best Local Similarity
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PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,364
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,370
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
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NAME/KEY: misc feature
LOCATION: (831)
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GAGAGAGCAGAGGTGGGCAGGCCCTTTTGATTAATGTATCATTCTTGAATGCAAGCTTCA
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                                                                                                              AAATCCGGGTATGCCGGGTGAGAATGAGCAGGACTAACACCTGGGTGTCATGGCAAGCCT
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                                                                      AAATCCGGGTATGCCGGGTGAGAATGAGCAGGACTAACACCTGGGTGTCATGGCAAGCCT
                                                                                                                                                             GAGAGAGCAGAGGTGGGCCCTTTTGATTAATGTATCATTCTTGAATGCAAGCTTCA
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APPLICANT: SUMA, MAKIKO
APPLICANT: ASMA, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
APPLICANT: ABURATANI, HIROYUKI
FILE REFERENCE: 064335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
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US-10-017-161-1041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOPTWARE: PatentIn Ver. 2.1
SEQ ID NO 1041
LENGTH: 39703
                                                                                                          FEATURE:
                                                                                                                                                                                                                         FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: CDS
LOCATION: (16990)..(17067)
                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: CDS
LOCATION: (15377)..(15440)
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NAME/KEY: CDS
LOCATION: (14506)..(14748)
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                                                    NAME/KEY: CDS
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NAME/KEY: CDS
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                                                                     FEATURE
                                                                                                                                                LOCATION: (19258)..(19390)
                                                                                                                                                                                                         LOCATION: (18612)..(18762)
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                               LOCATION: (20987)..(21167)
                                                                                        LOCATION: (20773)..(20889)
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Matches 139; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: AKIYAMA, YUTAKA
APPLICANT: AKIYAMA, HIROYUKI
APPLICANT: ABURATANI, HIROYUKI
TITLE ONE GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSE
APPLICANT: AKIYAMA, YUI
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: JP 2001-246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 10/017,161 PRIOR FILING DATE: 2001-12-18
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LOCATION: (23354)..(23497)
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LOCATION: (39365)..(39503)
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LOCATION: (23003)..(23131)
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                                                                                                                                                                                                                                                                                        FEATURE:
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LOCATION: source
                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                          NAME/KEY:
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NAME/KEY: CDS
                                   COCATION:
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                                   (5787) .. (5888)
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                                                                                              [4517] .. (4687)
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                                                                                                                   GENERAL INFORMATION:
APPLICANT: Williams, Amanda
APPLICANT: Boland, Joseph F.
APPLICANT: Lord, Reginald V.
APPLICANT: Alvarez, Chris
APPLICANT: Wetzel, Jon C.
APPLICANT: Scherf, Uwe
                                                                                                                                                                                                                                                                 Sequence 1102, Application US/10240425
Publication No. US20040033502A1
                                                                                                                                                                                                                                                GENERAL
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    APPLICANT: Scherf, Uwe
APPLICANT: Vockley, Joseph G.
APPLICANT: Vockley, Joseph G.
TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
FILE REFERENCE: 44921-5026
CURRENT APPLICATION NUMBER: U$/10/240,425
CURRENT FILING DATE: 2002-09-30
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: PCT/US01/09847
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LOCATION: (39365)..(39503)
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Local Similarity 93.9%;
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CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 688
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                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
FEATURE:
FMAME/KEY: misc_feature
LCCATION: {1)...(97247)
COTHER INFORMATION: n = A,T,C or G
US-10-087-192-688
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Publication No.
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SEQ ID NO 1102
LENGTH: 134292
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MORRIS, David W.
APPLICANT: Engelhard, Bric K.
RITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 60/193,446
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 1588
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                                                       33929 GTCTCGATCTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACA 33870
                                                                                                                                          33989 CGGCTAATTTTTTGTATTTTTTTTTTAGTAGACACGGGGTTTCACCGTGTTAGCCAGGATG
122 GGCATGAGCCACTGCGGCCCAGCCGGTCTTTTTAAACATTCCCC 164
                                                                                                                                                                                                                              143;
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                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                15.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                            Score 131; DB 13; Length 97247; Pred. No. 6.5e-31; 0; Mismatches 20; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 133.6; DB 13; Length 134292; Pred, No. 1.1e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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33869 GGCGTGAGCCACCGCGCCCAGCCCCCTTTTCTAACCTCTCTCC 33827

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APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lew, Simon M.
APPLICANT: Aljona, Anibal A.
TITLE OF INVENTION: MOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: MOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: MOVEL LOW DENSITY USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
TITLE OF INVENTION: ATHEROSCLEROSIS
TITLE OF INVENTION: ATHEROSCLEROSIS
TITLE OF INVENTION: ATHEROSCLEROSIS
CURRENT APPLICATION NUMBER: US/09/976,740
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR TILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR TILING DATE: 1997-66-03
NUMBER OF SEQ ID NOS: 53
NUMBER OF SEQ ID NOS: 53
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lews, Robert S.
APPLICANT: Lew, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: APPLICATION NUMBER: US/10/671,242
CURRENT APPLICATION NUMBER: US/09/616,289
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1997-11-26
PRIOR PILING DATE: 1997-11-27
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; ORGANISM: Homo sapiens
US-09-976-740-51
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US-10-671-242-51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 140; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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Publication No. US20040049A1
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22255
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89.7%;
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Publication Mo. US2002011
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Roberi
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CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR PILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR PILING DATE: 1996-11-27
PRIOR PILING DATE: 1996-11-27
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PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 51
LENGTH: 22255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 15.0%; Score 130.4; DB 13; Length Best Local Similarity 89.7%; Fred. No. 5.1e-31; Matches 140; Conservative 0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-0044001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: US 60/048,547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1997-06-03
                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 22255
                                                                                                                                                                                                                                                            y match
Local Similarity 89.7%;
tes 140; Conservative
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                                                 7406 CGATCTCTTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCT 7465
                                                                                                                                                            7346 TTTTTTTTTTTTTTTTTTTAGTÄGAGACGGGGTTTCACCGTGTTAGCCAGGAIGGTCT
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126 TGAGCCACTGCGCCCAGCCGGTCTTTTTAAACATTC 161
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                                                                                                     66 CGAACTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCA 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGAACTCCTGACCTCGTGATCCGCCCGCCTCCGGCCTCCCAAAGTGCTGGGATTACAGGCA 125
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                                                                                                                                                                                               TITITITITITITAAGIAGAGAIGGGGTTTCACCGIGITAGCCAGGAIGGTCI 65
                                                                                                                                                                                                                                                                    Score 130.4; DB 14; Length 22255; Pred. No. 5.1e-31; 0; Mismatches 16; Indels 0;
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APPLICANT: Arjona, Animal A.
APPLICANT: Arjona, MANDEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: MOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: AFMEROSCLEROSIS
FILE REPERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,523
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR PRICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-66-03
NUMBER: US 50/048,547
PRIOR FILING DATE: 1997-66-03
NUMBER: US 50/048,547
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US-10-616-187-51
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Publication No. US2004001366BA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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APPLICANT: Lees, Rober
APPLICANT: Law, Simon
APPLICANT: Arjona, Ani
APPLICANT: Lees, Robert S.
APPLICANT: Lew, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTSIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: APPLICATION APPLICATION NUMBER: US/10/616,187
CURRENT APPLICATION NUMBER: US/09/616,289
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-09
PRIOR FILING DATE: 2000-07-09
PRIOR FILING DATE: 2000-07-09
PRIOR FILING DATE: 2000-07-09
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lees, Arn M. APPLICANT: Lees, Rober
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ORGANISM: Homo sapiens
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Law, Simon W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGAGCCACCACGCCTGGCCTATTTATTTATTTATTTC 7501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.0%; Score 130.4; DB 14; Length 22255; 89.7%; Pred. No. 5.1e-31; ative 0; Mismatches 16; Indels 0;
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US-10-616-187-51
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RESULT 14
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Publication No. US20030166203A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Fast
SEQ ID NO 3
LENGTH: 20951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 51
                                                                                                                                                                                                                                                                                                                      Query Match 14.9%; Score 129.4; DB 10; Length 20951; Best Local Similarity 87.1%; Pred. No. 1.1e-30; Matches 142; Conservative 0; Mismatches 21; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-66-03
NUMBER OF SEQ ID NOS: 53
SOPTWARE: FastSEQ for Windows Version 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PILE REFERENCE: CL001165
CURRENT APPLICATION NUMBER: US/09/805,455
CURRENT FILING DATE: 2001-03-14
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Human
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                                                             17156 GAGCCACCGCGCCCGGCCTGTCCTTTATTATCCCACCAC 17114
                                                                                                                                               17216 GATCTCCTGACCTCGTGATCCGCCCGCCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGT 17157
                                                                                                                                                                                                                                    17276 TITTTTTTTTTTTTTTAGTAAAGATGGGGTTTTCACCGTGTTAGCCAGGATGGTCTC
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                                                                                                     127 GAGCCACTGCGCCCAGCCGGTCTTTTTAAACATTCCCCAGGAC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 CGAACTCCTGACCTCGTGATCCGCCCGCCCTCCCCAAAGTGCCTGGGATTACAGGCA 125
                                                                                                                                                                         67 GAACTCCTGACCTCGTGATCCGCCCCCCCCCCCCCCAAAGTGCTGGGGATTACAGGCAT 126
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89.7%;
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, Sequence 3, Application US/10678140 ; Publication No. US20040082772A1 ; GENERAL INFORMATION:

US-10-678-140-3/C

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Sequence 165977, Application US/10027632

| Publication No. US20020198371A1
| GENERAL IMFORMATION:
| APPLICANT: Wang, David G.
| TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
| TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
| TITLE OF INVENTION: Polymorphisms in the Human Genome
| FILE REFERENCE: 108627.129
| CURRENT APPLICATION NUMBER: US/10/027,632
| CURRENT PILING DATE: 2000-07-12
| PRIOR APPLICATION NUMBER: US 60/218,006
| PRIOR APPLICATION NUMBER: US 60/198,676
| PRIOR APPLICATION NUMBER: US 60/193,493
| PRIOR APPLICATION NUMBER: US 60/193,493
| PRIOR APPLICATION NUMBER: US 60/193,493
| PRIOR APPLICATION NUMBER: US 60/185,218
| PRIOR APPLICATION NUMBER: US 60/185,218
| PRIOR APPLICATION NUMBER: US 60/185,363
| PRIOR APPLICATION NUMBER: US 60/187,363
                                                                                                                                                                                                           : LENGTH: 827

: TYPE: DNA

: ORGANISM: Human

US-10-027-632-165977
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US-10-027-632-165977/c
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Matches 142; Conserv
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                                                                                                                                                                                                                                                                                                                   SEQ ID NO 165977
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TITLE OF INVENTION: SIGLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CLOO1165DIV
CURRENT FAPLLCATION NUMBER: US/10/678,140
CURRENT FILLING DATE: 2003-10-06
NUMBER OF SEQ ID NOS: 8
SOFTMARE: FastSEQ for Windows Version 4.0
                                                                                                          Matches
                                                                                                                                                            Query Match
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PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
RUMBER OF SEQ ID NOS: 325720
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TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                   Local
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6 TTTTTTTTTTTTTTTTAAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATGGTCT 65
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                                                                                                          Conservative
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                                                                                                       14.9%; Score 128.8; DB 13; Length 827; 91.9%; Pred. No. 3.7e-31; tive 0; Mismatches 12; Indels 0;
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                                     126 TGAGCCACTGCGCCCAGCCGGTCTTTT 153
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Search completed: May 24, 2004, 16:51:23 Job time : 361 secs

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
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7.4 819
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7.0 1986
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6.7 92139
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                                              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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7.6 148567
7.4 460
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/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-09-918-686-25
US-09-918-686-25
US-09-918-686-13
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US-09-9569-852B-1
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6776.654 Million cell updates/sec
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Sequence 13, Appl
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6.3 3.06 4 US-09 6.3 3.20 1 US-08 6.3 3.20 1 US-08 6.3 489 4 US-09 6.3 1268 4 US-09 6.3 1268 4 US-09 6.3 1280 4 US-09 6.3 2280 4 US-09 6.3 3280 4 US-09 6.3 3742 1 US-09 6.3 3742 1 US-09	6.3 320 1 US-09-621-976-11059 Sequence 6.3 320 1 US-08-759-873-5 Sequence 6.3 476 4 US-08-759-873-5 Sequence 6.3 476 4 US-09-621-976-17689 Sequence 6.3 480 4 US-09-621-976-10615 Sequence 6.3 480 4 US-09-621-976-652 Sequence 6.3 489 4 US-09-621-976-652 Sequence 6.3 856 4 US-09-621-976-8994 Sequence 6.3 1268 4 US-09-369-247-42 Sequence 6.3 1268 4 US-09-369-247-42 Sequence 6.3 1268 4 US-09-369-157-171-3 Sequence 6.3 1269 4 US-09-705-321 Sequence 6.3 2280 4 US-09-736-457-321 Sequence 6.3 2280 4 US-09-614-1248-321 Sequence 6.3 2280 4 US-09-614-1248-321 Sequence 6.3 3742 1 US-08-694-915-5 Sequence 6.3 3742 1 US-08-694-915-5 Sequence 6.3 3742 1 US-08-694-915-5 Sequence 6.3 3820 4 US-09-797-908-3 Sequence 6.3 Sequence 6.3 3742 1 US-08-694-915-5 Sequence 6.3 Sequence	45	44	بي	42	44	40	9	38	37	36	3	34	B B	32	Зμ	30	29	28
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		US-09-797-908-3	US-08-694-915-5	US-09-589-184-321	US-09-671-325-321	US-09-614-124B-321	US-09-736-457-321	US-09-702-705-321	US-09-050-159-128	US-08-157-171-3	-09-369-247	US-09-288-143-47	US-09-621-976-8994	US-09-621-976-652	US-09-621-976-10615	US-09-621-976-17689	US-08-759-873-5	-08-625	60-

ALIGNMENTS

GENERAL INFORMATION: APPLICANT: YE, Jane et al TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREOF FILE REFERENCE: CL001160 US-09-801-876B-3 US-09-801-876B-3 NUMBER OF SEQ ID NOS: 8 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3 LENGTH: 148567 Sequence 3, Application US/09801876B Patent No. 6492155 CURRENT APPLICATION NUMBER: US/09/801,876B CURRENT FILING DATE: 2001-03-09 ORGANISM: Human FEAJURE: NAMS/KEY: misc_feature LOCATION: {1)...(148567) OTHER INFORMATION: n = A,T,C or G TYPE: DNA

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                                                         GENERAL INFORMATION:
APPLICANT: YE, Jame et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THERBOF
FILE REFERENCE: CL001150DIV
                                                                                                                                                                                  Sequence 3, Application US/10254869
Patent No. 6653117
CURRENT APPLICATION NUMBER: US/10/254,869
CURRENT FILING DATE: 2002-09-26
NUMBER OF SEQ ID NOS: 8
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Best Local Similarity 100.0%; Pred. No. 1.2 Matches 66; Conservative 0; Mismatches

7.6%; Score 66; DB 4; Le 100.0%; Pred. No. 1.2e-20;

Length 148567; Indels

0;

Gaps

Query Match

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GENERAL INFORMATION:
APPLICANT: Brunkow, Mary
APPLICANT: Proll, Sean
APPLICANT: Proll, Seri
APPLICANT: Scachling-Hampton, Karen
ITILE OF INVENTION: METHODS FOR IDENTIFYING
ITILE OF INVENTION: GENOMIC DELETIONS
FILE REFERENCE: 240083.515
CURRENT APPLICATION NUMBER: US/09/918,686
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 105
                                                                                                                                                                                 US-09-337-171-13/c

; Sequence 13, Application US/09337171
; Patent No. 6262249
; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-918-686-26
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US-09-918-686-26
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              APPLICANT: Kennedy, Giulia C
TITLE OF INVENTION: PANCERATIC CANCER GENES
FILE REFERENCE: 200130.454
CURRENT APPLICATION NUMBER: US/09/337,171
CURRENT FILING DATE: 199-06-21
NUMBER OF SEQ ID NOS: 15
SOPTWARE: PASESEQ for Windows Version 3.0
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 26, Application US/09918686 Patent No. 6475739
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LENGTH: 819
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LOCATION: (1)...(148567)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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nilarity 100.0%; Pred. No. 1.3e-29;
Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.2e-20;
ive 0; Mismatches 0; Indels 0
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APPLICANT: Brunkow, Mary
APPLICANT: Proll, Sean
APPLICANT: Proll, Seyan
APPLICANT: Staehling-Hampton, Karen
TITLE OF INVENTION: METHODS FOR IDENTIFYING
TITLE OF INVENTION: GENOMIC DELETIONS
FILE REFERENCE: 24008.515
CURRENT APPLICATION NUMBER: US/09/918,686
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
TENTIFIC 2012
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US-09-773-459-13/c
; Sequence 13, Application US/09773459
prent No. 6664054
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US-09-918-686-1
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                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09918686 Patent No. 6475739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; P
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Best Local :
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TITLE OF INVENTION: PANCREATIC CANCER GENES
FILE REFERENCE: 200130.454
CURRENT APPLICATION NUMBER: US/09/773,459
CURRENT FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: US 09/337,171
PRIOR FILING DATE: 1999-06-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 15
                                                                                   LENGTH: 92
TYPE: DNA
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TYPE: DNA
ORGANISM: Homo sapien
PEATURE:
NAME/KEY: misc_feature
LOCATION: 7043, 8369, 8401
                                                               ORGANISM: Homo sapiens
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                                                                                                       92139
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US-09-776-976-7/c
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                                                                                                                                                                                                                                                                                  GENERAL.
                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: GONG, Fangcheng et al
TITLE OF INVENTION: ISOLATED HUMAN DEHYDROGENASES, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING THESE HUMAN DEHYDROGENASES, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOOMS4
CURRENT APPLICATION NUMBER: US/09/740,028A
CURRENT FILING DATE: 2000-12-20
CURRENT FILING DATE: 2000-12-20
CURRENT FILING DATE: 2000-12-20
CURRENT FILING DATE: 2000-12-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence 3, Application US/09740028A
Patent No. 6410289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 64;
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                                                   CURRENT APPLICATION NUMBER: US/09/776,976
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/758,055
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR FILING DATE: 2000-01-14
                                                                                                                                                                 APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
FILE REFERENCE: 76.US4.REG
                                                                                                                                                                                                                      APPLICANT: Fruebis, Joachim
APPLICANT: Erickson, Mary F
APPLICANT: Yen, Frances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: n = A, T, C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(19806)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGIH: 19806
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APPLICATION NUMBER: US 60/198,087
FILING DATE: 2000-04-13
APPLICATION NUMBER: US 60/299,881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2440 CCAC 2443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2380 CTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAG 2439
                                                                                                                                                                                                                                                                                INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 326 C 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 CCAC 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 C 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 TGGTCTCGAACTCCTGACCTCGTGATCCGCCCCCCCCGGCCTCCCAAAGTGCTGGGATTA
                                                                                                                                                                                                                                                                                                  7, Application US/09776976
5, 6566332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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Pred. No.
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SOFTWARE: Patent.pm
SEQ ID NO 7
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NUMBER OF SEQ ID NOS: 7
                                                          NAME/KEY: primer bind
LOCATION: 16191..16211
                                                                                                                       OTHER INFORMATION: 9-12.rp complement NAME/KEY: primer_bind LOCATION: 15759..15776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFO
NAME/KEY: primer bind LOCATION: 16982...17001
                                                                                                     OTHER INFORMATION: 99-14405.pu
                                                                                                                                                                                                                              OTHER INFORMATION: 9-12.pu
                                                                                                                                                                                                                                                NAME/KEY: primer_bind
LOCATION: 15073..15092
                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: primer bind LOCATION: 10990..11008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: allele
LOCATION: 17170
                                      OTHER INFORMATION: 99-14405.rp complement
                                                                                                                                                                                                        NAME/KEY: primer_bind
                                                                                                                                                                                                                                                                                                             NAME/KEY: primer_bind
LOCATION: 11423..11442
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LOCATION: 3928..3946
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LOCATION: 3528..3545
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LOCATION: 15863
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                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: 99-14387.pu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: 9-27.pu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: 99-14405-105 : polymorphic base A or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: 9-12-428 : polymorphic base A or
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LOCATION: 15500
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LOCATION: 15196
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NAME/KEY: allele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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OCATION: 20560..20966
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; NAME/KEY: primer_bind; LCATION: 17171...17189
corner INFORMATION: 9-16-189.mis complement US-09-776-976-7
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PRIOR APPLICATION NUMBER: US 09/776,976
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/758,055
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR APPLICATION NUMBER: US 60/198,087
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Yen, Frances
APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OBJ. Globular Head and Uses Thereof for Decreasing Body Mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/176,228 PRIOR FILING DATE: 2000-01-14
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CURRENT FILING DATE: 2001-07-19
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                                                                                                   NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: 5' regulatory region NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEATURE:
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: exon
                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: exon
LOCATION: 1514
                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: exon
                                               NAME/KEY: allele
LOCATION: 15196
                                                                                                                                                                                                                                                                                                       OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
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                                                                                                                                           OTHER INFORMATION:
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OCATION:
                                  THER INFORMATION:
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                                                                                                                                                                            RAME/KEY: allele
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5, 6579852
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                   allele
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                                                                                                                                                                                                                                                                                     feature
                                                                                                                                                                                           9-27-261 : polymorphic base G
                                                                                                                                                                                                                                                                                                       exon
                                9-12-124 : polymorphic base
                                                                                    9-12-48 : polymorphic base C or
                                                                                                                                        99-14387-129 : polymorphic base A or
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100.0%; Pr
                                                                                                                                                                                                                                                 regulatory region
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Pred. No. 6.5e-18;
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or
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NAME/KEY: primer bind LOCATION: 3768.3786 OTHER INFORMATION: 9-27-261.mis NAME/KEY: primer_bind
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LOCATION: 15488..15512
OTHER INFORMATION: 9-1:
                                                                                                                                                                                                                                                                                     LOCATION: 15851..15875
OTHER INFORMATION: 99-14405-105.probe
                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_binding
LOCATION: 15851..15875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_binding
LOCATION: 15415..15439
                                                        OTHER INFORMATION: 9-27-261.mis complement
                                                                                                                                                                                                                     LOCATION: 17158..17182
OTHER INFORMATION: 9-16-189.probe
                                                                                                                                                                                                                                                                        NAME/KEY: misc_binding
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LOCATION: 15184..15208
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LOCATION: 15108..15132
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LOCATION: 11106..11130
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LOCATION: 11423..11442
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OTHER INFORMATION: 9-27.pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: primer bin
LOCATION: 3528..3545
                        NAME/KEY: primer_bind
LOCATION: 11099...1111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_binding LOCATION: 3775..3799
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LOCATION: 17384..17402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THER INFORMATION: 9-16.pu
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OCATION: 16191..16211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: 99-14405.pu
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WCATION: 15759..15776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: 99-14387.rp complement
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LOCATION: 3928..3946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: 9-16-189 : polymorphic base deletion of A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: 99-14405-105 : polymorphic base A or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: 9-12-428 : polymorphic base A or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OCATION: 15500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THER INFORMATION: 9-12-355 : polymorphic base G or T
INFORMATION: 99-14387-129.mis
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                                                                                      Matches
                                                                                                                              Query Match
                                                                                                         Best Local Similarity 100.0%;
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NAME/KEY: primer_bind
LOCATION: 15121..15139
                                                                                                                                                                                                 OTHER INFORMATION: 9-16-189.mis complement
                                                                                                                                                                                                                    NAME/KEY: primer bind LOCATION: 17171. 1718
                                                                                                                                                                                                                                                                                 NAME/KEY: primer_bind
LOCATION: 17151..17169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: 9-12-355.mis NAME/KEY: primer_bind LOCATION: 15428..15446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: 9-12-124 mis complement NAME/KEY: primer_bind LOCATION: 15408.15426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: 99-14387-129.mis complement NAME/KEY: primer_bind LOCATION: 15101..15119
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LOCATION: 11119..11137
                                                                                                                                                                                                                                                                 OTHER INFORMATION: 9-16-189.mis
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                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: primer_bind
LOCATION: 15864..15882
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LOCATION: 15844..15862
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LOCATION: 15501..15519
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LOCATION: 15481..15499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: 9-12-428.mis complement
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10046 GTGATCCGCCCCCCCCCCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCC 9987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION: 9-12-48.mis
                                     81 GTGATCCGCCCCCGCCTCCCCAAAGTGCTGCGATTACAGGCATGAGCCACTGCGCCC 140
                                                                                    60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer_bind
15197..15215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer_bind
15177..15195
                                                                                      Conservative
                                                                                                         6.9%; Score 60; DB 4;
L00.0%; Pred. No. 6.5e-
                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement
                                                                                                           6.5e-18;
                                                                                                                                Length 20966;
                                                                                        Indels
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                                                                                        Gaps
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RESULT 10

US-09-569-852B-1/c

US-09-569-852B-1/c

Sequence 1, Application US/09569852B

Fatent NO. 6582909

GENERAL INFORMATION:
APPLICANT: Bhisin, Bernard

APPLICANT: Denison, Blake
APPLICANT: Cenison, Blake
APPLICANT: Penison, Blake
APPLICANT: Penison, Blake
APPLICANT: Cenison, Blake
APPLICANT: Penison, Blake
FILLE REFERENCE: GEN-T113XC2
CURRENT APPLICATION NUMBER: US/09/569,852B
CURRENT FILLING DATE: 2002-03-12

PRIOR APPLICATION NUMBER: PCT/IB99/01858

PRIOR FILLING DATE: 1999-11-04

PRIOR APPLICATION NUMBER: US 60/119,593

PRIOR APPLICATION NUMBER: US 60/119,593

PRIOR APPLICATION NUMBER: US 60/107,113

PRIOR FILLING DATE: 1999-02-10

PRIOR FILLING DATE: 1999-11-04

PRIOR APPLICATION NUMBER: US 60/107,113

PRIOR FILLING DATE: 1998-11-04

PRIOR APPLICATION NUMBER: US 60/107,113

PRIOR FILLING DATE: 1998-11-04

PRIOR FILLING DATE: 1998-11-04

PRIOR APPLICATION NUMBER: US 60/107,113

PRIOR FILLING DATE: 1998-11-04

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PRIOR APPLICATION NUMBER: US 60/107,113

PRIOR FILLING DATE: 1998-11-04

PRIOR APPLICATION NUMBER: US 60/107,113

PRIOR FILLING DATE: 1998-11-04

PRIOR APPLICATION NUMBER: US 60/107,113

PRIOR PRIOR PRIOR APPLICATION NUMBER: US 60/107,113

PRIOR PRIOR PRIOR APPLICATION NUMBER: US 60/107,113
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SEQ ID NO 1
LENGTH: 20966
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: primer_bind
LOCATION: (15051)..(15069)
OTHER INFORMATION: 17-35-306.mis complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: primer bind
LOCATION: (15031)..(15049)
OTHER INFORMATION: 17-35-306.mis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: primer_bind
LOCATION: (14796)..(14814)
OTHER INFORMATION: 17-35-71.mis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: primer bind
LOCATION: (14758)..(14776)
OTHER INFORMATION: 17-34-915.mis complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAMB/KEY: primer bind
LOCATION: (14683)..(14701)
OTHER INFORMATION: 17-34-860.mis
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                                             LOCATION: (15844)..(15862)
OTHER INFORMATION: 99-14405-105.mis
                                                                                                                    LOCATION: (15791)..(15809)
OTHER INFORMATION: 17-36-120 mis complement
                                                                                                                                                                                                 LOCATION: (15771)..(15789)
OTHER INFORMATION: 17-36-120.mls
                                                                                                                                                                                                                                                                    NAME/KBY: primer_bind
LOCATION: (15881)..(15699)
OTHER INFORMATION: 17-36-47.mis complement
                                                                                                                                                                                                                                                                                                                                                 LOCATION: (15661)..(15679)
OTHER INFORMATION: 17-36-47.mis
                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (15501)...(15519)
OTHER INFORMATION: 9-12-428.mis complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (15481)..(15499)
OTHER INFORMATION: 9-12-428.mis
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LOCATION: (15428)..(15446)
OTHER INFORMATION: 9-12-355.mis complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: primer_bind
LOCATION: {15101}..(15119)
OTHER INFORMATION: 9-12-48.mis
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LOCATION: (14816) .(14834)
OTHER INFORMATION: 17-35-71.mis_complement
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LOCATION: (14738)..(14756)
OTHER INFORMATION: 17-34-915.mis
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LOCATION: (14703).(14721)
OTHER INFORMATION: 17-34-860.mis complement
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                                                                                            NAME/KEY: primer bind
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OTHER INFORMATION: 9-12-355.mis
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OTHER INFORMATION: 9-12-124.mis complement
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OTHER INFORMATION: 9-12-124.mis
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OTHER INFORMATION: 9-12-48.mis complement
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NAME/KEY: primer_bind
LOCATION: (15864)..(15882)
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NAME/KEY: primer_bind
LOCATION: (17151).(17169)
OTHER INFORMATION: 9-16-189.mis
NAME/KEY: primer_bind
LOCATION: (17171)..(17189)
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LOCATION: (18470)..(18488)
OTHER INFORMATION: 17-38-349.mis
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OTHER INFORMATION: 17-37-629.mis complement
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LOCATION: {17810}...{17828}
OTHER INFORMATION: 17-37-629.mis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: 9-16-189.mis complement
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LOCATION: (926)..(944)
OTHER INFORMATION: 17-30-216.mis
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OTHER INFORMATION: 17-38-349.mis complement
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LOCATION: (18490)..(1:
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LOCATION: {18012}..(18030)
OTHER_INFORMATION: 17-37-811.mis complement
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LOCATION: (17992)..(1)
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LOCATION: {17830}...(1
                                    NAME/KEY: primer_bind
LOCATION: (10638)..(10656)
OTHER_INFORMATION: 17-32-24.mis complement
                                                                                                                                                                                                                                                            NAME/KEY: primer_bind
LOCATION: (5211)...(5229)
OTHER INFORMATION: 17-31-413.mis complement
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LOCATION: (5096)..(51)
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LOCATION: (3719)..(37
                                                                                                                                          NAME/KEY: primer_bind
LOCATION: (10618)..(10
                                                                                                                                                                                                             NAME/KEY: primer_bind
LOCATION: (5364)..(53
                                                                                                                                                                                                                                                                                                                                    LOCATION: (5191)..(5209)
OTHER INFORMATION: 17-31-413.mis
                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: primer_bind
LOCATION: (5191)..(52)
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OTHER INFORMATION: 17-31-298.mis
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LOCATION: (3788)..(38
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LOCATION: (3754)..(37
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OTHER INFORMATION: 9-27-211.mis complement
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LOCATION: (3739)..(37
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DTHER INFORMATION: 9-27-211.mis
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LOCATION: (946)..(964
                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (5096)..(5114)
OTHER INFORMATION: 17-31-298.mis complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (3788)..(3806)
DTHER INFORMATION: 9-27-261.mis complement
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WOCATION: (3768)..(37
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AMB/KEY: primer bind
OCATION: (11020)...(1)
                                                                                                                 OCATION: (10618)..(10636)
THER INFORMATION: 17-32-24.mis
                                                                                                                                                                                    OCATION: (5364)..(5385)
THER INFORMATION: 17-31.rp complement
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THER INFORMATION: 9-27-246.mis complement
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INFORMATION: 17-37-811.mis
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LOCATION: (11020)..(11038)
OTHER INFORMATION: 99-14387-50.mis

(11038)

NAME/KEY: primer_bind LOCATION: (11040)..(1)

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US-09-621-976-15373; Sequence 15373, Application US/09621976; Patent No. 6639063;
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                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-621-976-15373
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                                                                                                                                                                                                                                FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 15373
LENGTH: 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (20560)...(20966)
OTHER INFORMATION: 3' regulatory region
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LOCATION: (13974)...(13992)
OTHER INFORMATION: 17-33-TGAGACT.mis complement
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LOCATION: (11169)...(11187)
OTHER INFORMATION: 99-14387-199.mis
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LOCATION: (11119)..(11137)
OTHER INFORMATION: 99-14387-129.mis complement
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LOCATION: (11099)..(11117)
OTHER INFORMATION: 99-14387-129.mis
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LOCATION: (13954)..(13972)
OTHER_INFORMATION: 17-33-TGAGACT.mis
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LOCATION: (11189)...(1)
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OTHER INFORMATION: 99-14387-50.mis complement
                                                                                                                                                                                                                  TYPE: DNA
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OTHER INFORMATION:
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OTHER INFORMATION:
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DTHER INFORMATION: 99-14387-199.mis complement
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                                                                                                           Local Similarity 100.0%;
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51
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ACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCAC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                Jobert, S.
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Conservative 0;
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100.0%; Pred. No. 6.5e-18;
                                                                                                         6.7%; Score 58; DB 4; Length 506; 100.0%; Pred. No. 6.6e-17;
                                                                                    0; Mismatches
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RESULT 12

NAME/KEY: allele

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                                               US-09-345-882-1
                                                                     RESULT 13
                                                                                                                                                                                                                                                                                                                       US-09-918-686-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Brunkow, Mary
APPLICANT: Proll, Sean
APPLICANT: Paeper, Bryan
APPLICANT: Staehling-Hampton, Karen
APPLICANT: Staehling-Hampton, Karen
TITLE OF INVENTION: METHODS FOR IDENTIFYING
TITLE OF INVENTION: GENOMIC DELETIONS
FILE REFERENCE: 240083.515
CURRENT APPLICATION NUMBER: US/09/918,686
CURRENT FILING DATE: 2001-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09918686 Patent No. 6475739 GENERAL INFORMATION:
Sequence 1, Application US/09345882 Patent No. 6399373
                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                   FEATURE: MISC_feature
LOCATION: 7043, 8369, 8401
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 92139
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                                                                                                                                        75299 GTGATCCGCCCCCCCCGGCCTCCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGC 75242
                                                                                                                                                                                 B1 GTGATCCGCCCCCCCCCCCCCCCCAAAGTGCTGCGAATTACAGGCATGAGCCACTGCGC 138
                                                                                                                                                                                                                                 58;
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SOFTWARE:
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NAME/KEY: Allele
72794
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CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR APPLICATION NUMBER: 1998-12-10
NUMBER OF SEQ ID NOS: 140
                                                                                      PEATURE:
NAME/KEY: allele
NAME/KEY: 90842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
                                                                                                                                                                                                        LOCATION: 72794
OTHER INFORMATION: 5-124-273 : FEATURE:
                FEATURE:
NAME/KEY: allele
LOCATION: 93714
                                                                                                                                              LOCATION: 88073
OTHER INFORMATION:
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OTHER INFORMATION:
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NAME/KEY: allele
LOCATION: 134374
OTHER INFORMATION:
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LOCATION: 99098
OTHER INFORMATION:
NAME/KEY: allele
LOCATION: 72771..72817
                                       OTHER INFORMATION:
                                                  NAME/KEY: allele
LOCATION: 72771.
                                                                                        LOCATION: 160031
OTHER INFORMATION: 5-148-352
                                                                                                                    NAME/KEY: allele
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 134362
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OTHER INFORMATION:
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OTHER INFORMATION:
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NAME/KEY: allele
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LOCATION: 108308
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OTHER INFORMATION:
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OTHER INFORMATION:
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NAME/KEY: allele
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OTHER INFORMATION: 5-130-276
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LOCATION: 146345
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                                       polymorphic fragment 5-124-273 SEQ ID30
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LOCATION: 88050..88096
OTHER INFORMATION: polymorphic
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                                                     NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymo
                                                                                                                                                                                                             NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: pol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: allele
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LOCATION: 93690.
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LOCATION: 93690..93736
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LOCATION: 90819..90865
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OTHER INFORMATION:
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LOCATION: 90819..90865
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OTHER INFORMATION:
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LOCATION: 99094...
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OTHER INFORMATION:
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  OTHER INFORMATION: polymorphic
               NAME/KEY: allele
LOCATION: 106918.
                                           FEATURE:
                                                                                                          OTHER INFORMATION:
                                                                                                                                  NAME/KEY: allele
                                                                                                                                                            OTHER INFORMATION:
                                                                                                                                                                                    NAME/KEY: allele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KBY: allele
LOCATION: 97130..97177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OCATION:
                                                                                                                                                                                                                                                                                                                                OCATION:
                                                                                                                                                                                                                                                                                                                                              WAME/KEY: aliele
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                                                                                                                                                                                                                                                                                                                                  99075..99121
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                                                                                                                                                                                                                                                                                 .99140
                                                                                                                       ..103828
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                ..106966
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                                                      polymorphic
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  fragment 5-133-375 SEQ ID58
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                                                         SEQ
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                                                                                                             SEQ ID57
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OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38

108084..108130

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Sequence 10, Application US/09593995
Patent No. 6406888
GENERAL INFORMATION:
APPLICANT: Cocklin, Darrell C.
APPLICANT: Gao, Zeren
TITLE OF INVENTION: HELICAL CYTOKINE ZALPHA
FILE REFERENCE: 99-38
CURRENT FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: 06/139,121
PRIOR FILING DATE: 1999-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Jobert, S.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTS and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 11454
                                                                                                                                                                                                                                                     RESULT 15
US-09-593-995-10/c
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 58;
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Best Local S
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NAME/KEY: misc_feature
LOCATION: 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: allele
LOCATION: 108127..108177
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OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153473 TGATCCGCCCGCCCCGCCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCC 153530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                              94 AACTCCTGACCTCGTGATCCGCCCGGCCTCGGCCTCCGAAAGTGCTGGGATTACAGGC 38
                                                                                                                                                                                                                                                                                                                                                                   68 AACTCCTGACCTCGTGATCCGCCCGCCCTCGGCCTCCCAAAGTGCTGGGATTACAGGC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 TGATCCGCCCCCCCCCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                       57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  6.6%; Score 57; DB 4; Indiarity 100.0%; Pred. No. 1.9e-16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                     HELICAL CYTOKINE ZALPHA33
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                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                          US-09-593-995-10
                                                                                                                                                                                          SOFTWARE: Fast
SEQ ID NO 10
LENGTH: 20598
                                                                                    Query Match 6.6%;
Best Local Similarity 100.0%;
                                                                     Matches
                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
242 CTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGGATTACAGGCAT 186
                                                                     57;
                  70 CTCCTGACCTCGTGATCCGCCCCCCCCCCCAAAGTGCTGGGGATTACAGGCAT 126
                                                                                                                                                                                                                            FastSEQ for Windows Version 3.0
                                                                     Conservative
                                                                                     6.6%; Score 57; DB 4; Length 20598; 100.0%; Pred. No. 1.5e-16;
                                                                     0; Mismatches
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Search completed: May 24, 2004, 18:20:09
Job time: 73 secs

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Result
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perfect score:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
     123
122.4
122.4
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  14.4 63000
14.3 161712
14.3 1712
14.3 16063
14.3 16063
14.3 16063
14.2 12672
14.2 12672
14.2 12672
14.1 174493
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867
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Listing first 45 summaries
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-616-289-51
US-09-671-317-485
US-09-671-317-485
US-09-611-781-15
US-09-611-781-15
US-09-611-781-5
US-09-611-781-5
US-09-611-781-5
US-09-611-781-5
US-09-801-052-3
US-10-020-121-3
US-10-020-121-3
US-09-497-855A-38
US-09-497-855A-38
US-09-128-155-16
US-09-128-155-17
US-09-128-155-11
US-09-128-155-11
US-09-128-155-11
US-09-128-155-11
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US-09-128-155-11
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6776.654 Million cell updates/sec
  Sequence 485, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 5, Appli Sequence 5, Appli Sequence 3, Appli Sequence 3, Appli Sequence 5, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 101, App Sequence 114, Appli Sequence 101, App Sequence 114, Appli Sequence 1144, Appli Sequence 1144, Appli Sequence 1
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13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.9	14.0	14.0	14.0
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US-09-740-041-3	US-09-875-114-2	US-09-875-223-2	PCT-US95-07201-43	US-08-367-841A-43	US-08-520-373D-4	PCT-US95-07201-10	US-08-367-841A-10	US-08-257-963B-10	US-09-755-665-46	US-09-589-184-321	US-09-671-325-321	US-09-614-124B-321	US-09-736-457-321	US-09-702-705-321	US-09-511-625B-5	US-09-511-625B-19	US-09-621-976-11392
Sequence 3, Appli	Sequence 2, Appli	Seguence 2, Appli	Seguence 43, Appl	•	Seguence 4, Appli	Sequence 10, Appl		Sequence 10, Appl	Sequence 46, Appl	321,		-	•	-	Sequence 5, Appri	Sequence 19, Appi	Sequence 11392, A

ALIGNMENTS

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CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR PILING DATE: 1997-11-26
PRIOR PILING DATE: 1997-11-26
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PASCSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-616-289-51
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SEQ ID NO 51
LENGTH: 22255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                 Matches 140;
                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                   7346 PTTTTTTTTTTTTTTTTTTTAGTAGAGACGGGTTTCACCGTGTTAGCCAGGATGGTCT
7466 TGAGCCACCACGCCTGGCCTATTTATTTATTTATTC 7501
                                                                                                 7406 CGATCTCTTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCT
                                              126 TGAGCCACTGCGCCCAGCCGGTCTTTTTAAACATTC 161
                                                                                                                         66 CGAACTCCTGACCTCGTGATCCGCCCGCCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCA 125
                                                                                                                                                                                                                                           6 TITTTTTTTTTTTTTTTTTTTAAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATGGTCT
                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                 15.0%; Score 130.4; DB 4
89.7%; Pred. No. 8.1e-30;
tive 0; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 22255;
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RESULT 2 US-09-671-317-485

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Sequence 485, Application US/09671317 Patent No. 6528260
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PRIOR APPLICATION NUMBER: PCT/IB00/00403
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: US 60/126,269
PRIOR APPLICATION NUMBER: US 60/126,269
PRIOR APPLICATION DATE: 1999-03-25
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APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS REI
FILE REFERENCE: 62.US3.CIP
CURRENT APPLICATION NUMBER: US/09/671,317
CURRENT FILING DATE: 2000-09-27
CURRENT FILING DATE: 2000-09-27
DRIOR APPLICATION NUMBER: US/09/536,178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1999-04-30 NUMBER OF SEQ ID NOS: 977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
LOCATION: 45214
OTHER INFORMATION: 10-289-201
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: 10-286-289 ; polymorphic base G or C NAME/KEY; allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: 5'regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 5466..7466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                    OTHER INFORMATION: 10-523-232
                                                                                                                                                      OTHER INFORMATION: 12-421-140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 45966..49312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: exon 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: exon
                                                                                                                                                                                                                        OTHER INFORMATION: 12-421-135
                                                                                                                                                                                                                                                                                        DIHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: 10-286-375 : polymorphic base A or
                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION:
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                                                                 NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45728..45965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   allele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chumakov,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .7725
                                                                                                                                                                                                                                                                                        12-425-57
                                                                                                                                                                                                                                                                                                                                                                                                                     10-286-345 : polymorphic base A or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ilya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marta
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                                                                                  : polymorphic base C
                     : polymorphic base C or T
                                                                                                                                                      : polymorphic base A
                                                                                                                                                                                                                        ; insertion of
                                                                                                                                                                                                                                                                                     polymorphic base A
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NAME/KEY: primer_bind
LOCATION: 7630..7648
OTHER INPORMATION: 10-:
NAME/KEY: primer_bind
LOCATION: 7650..7668
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LOCATION: 7276..7294
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LOCATION: 46032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: allele
LOCATION: 46029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: primer_bind
LOCATION: 7565..7583
OTHER INFORMATION: 10-286-289.mis complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: primer bind
LOCATION: 7545..7563
OTHER INFORMATION: 10-286-289.mis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: primer_bind
LOCATION: 21886..21906
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LOCATION: 17297..17314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: primer_bind LOCATION: 7676..7694
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LOCATION: 7600..7618
OTHER INFORMATION: 10-286-345.mis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: primer_bind
LOCATION: 46104..46123
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LOCATION: 36997..37015
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LOCATION: 36740..36758
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LOCATION: 21456..21474
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COCATION: 16839..16856
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: primer_bind
LOCATION: 7620..7638
OTHER INFORMATION: 10-286-345.mis complement
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LOCATION: 45705..45724
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COCATION: 45020..45037
                                                                                                                               NAME/KEY: primer_bind
LOCATION: 21576..21594
                                                                                                                                                                          OTHER INFORMATION: 12-425-57.mis complement
                                                                                                                                                                                                                                                          NAMB/KEY: primer_bind
LOCATION: 17239..17257
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                                                                                                                                                                                                                                                                                                   THER INFORMATION:
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                                                                                                           INFORMATION: 12-421-140.mis
                                           INFORMATION:
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primer bind
primer bind
21596..21614
21596..21614 complement
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17259..17277
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NAME/KEY: primer_bind LOCATION: 36952..36970 OTHER INFORMATION: 10-523-232.mis

NAME/KEY: primer_bind LOCATION: 36972..36990

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RESULT 3
US-09-780-172-18/c
; Sequence 18, Application US/09780172
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OTHER INFORMATION: 10-523-232.mis complement
NAME/KEY: primer bind
LOCATION: 45195. 45213
OTHER INFORMATION: 10-289-201.mis
NAME/KEY: primer bind
LOCATION: 45215. 45233
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LOCATION: 46030..46048
LOCATION: 10030..16018
OTHER INFORMATION: 10-290-326.mis complement
NAME/KEY: misc_binding
LOCATION: 7552..7576
OTHER INFORMATION: 10-286-289.probe
NAME/KEY: misc_binding
LOCATION: 7607.7631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: 10-290-326 probe
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LOCATION: 36959..36983
OTHER INFORMATION: 10-523-232.probe
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LOCATION: 21583..21607
OTHER INFORMATION: 12-421-140.probe
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OTHER INFORMATION: 12-425-57.probe
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NAME/KEY: misc_binding
LOCATION: 7637..7661
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LOCATION: 45722..45740
OTHER_INFORMATION: 10-290-37.mis
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LOCATION: 46010.46028
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LOCATION: 45742.45760
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                                                                                                                                                                                                                                                                                                                                                                                                                                            14.4%; Score 124.6; DB 4; Length 49312;
Local Similarity 90.5%; Pred. No. 7.9e-28;
les 133; Conservative 0; Mismatches 14; Indels 0;
                                                                                                                                                                                                                                         33634 TCCTGACCTCGTGATTTGCCCACCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGC 33693
                                                                                                                                                                                                                                                                                                                                                 33574 TTTTTTATATTTTTAAGTÁGÁGÁCGGGGTTTCÁCCGTGTTAGCCAGGACGGTCTCGATC 33633
                                                                                                                                      33694 CACTECECCCAGCAATTATTTTCAATC 33720
                                                                                                                                                                                          131 CACTGCGCCCAGCCGGTCTTTTAAAC 157
                                                                                                                                                                                                                                                                                                                                                                             11 TTTTTTTTTTTTAAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATGGTCTCGAAC 70
                                                                                                                                                                                                                                                                                             71
                                                                                                                                                                                                                                                                                             TCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGC 130
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Sequence 1, Application US/09426290
Patent No. 6410712
GENERAL INFORMATION:
APPLICANT: Berglind Ran Olafsdottir
APPLICANT: Jeffrey Gulcher
TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
FILL REFERENCE: 2345.2001-000
CURRENT APPLICATION UNMEER: US/09/426,290
CURRENT FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 24
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US-09-426-290-1/c
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                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 1
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   Matches
                              Query Match
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APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-ALPHA EXPRESSION
FILE REFERENCE: RTS-0159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/780,172
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Robert McKay
APPLICANT: Susan M. Freier
                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                     LOCATION:
                                                                                                  NAME/KEY: CDS
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   141;
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                   Similarity
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                                                                                  (128910)...(129139)
                                                                                                                                                                                    (110324)...(110439)
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                                                                                                                                                                                                                                                    (95252)...(95430)
                                                                                                                  (127009)...(127130)
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   Conservative
                 14.3%;
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0;
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                   Score 124.2; DB 4; Length 168575; Pred. No. 2.1e-27;
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     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
       28;
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       Indels
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       0; Gaps
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7 TYTTYTYTTTTTTTTTTTAAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATGGTCTC 66

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US-09-058-389A-12

GENERAL INFORMATION:

Belt,

Judith A.

APPLICANT: APPLICANT:

TITLE OF INVENTION: TITLE OF INVENTION:

NUMBER OF SEQUENCES:

COMPUTER READABLE FORM:

0760

Hackensack

Floor

New Jersey

USA

FILING DATE: A CLASSIFICATION:

APPLICATION NUMBER: US/09/ FILING DATE: April 9, 1998

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Sequence 12, Application US/09058389A Patent No. 6130065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "intron 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-013N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71067 TITTTTTGTATTTTTTTTAGTGGAGATGGGGTTTCACCGTGTTAGCCAGGATGGTCTG 71008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71007 GATCTCCTGATCTCGTGATCTGCCCGCCTCGGCCTCCCAAAGTGCTGCGATTACAGGCGT 70948
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586 GTCTCGATCTCCTGACCTCGTGATCCTCCCGGCCTCCGGCCTCCCAAAGTGCTGGGATTACA
                                                                                                                              526 CGCGGCTATTTTTTTTTTTTTTTAGTAGAGACGGGTTTCACCGTGTTAGCCAGGATG 585
                                                           62 GTCTCGAACTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACA 121
                                                                                                                                                                                   2 CGAGTTTTTTTTTTTTTTTTTTTAAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATG 61
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Patel, Divyen
Patel, Divyen
Patel, Divyen
ROBENZYLMERCAPTOPURINERIBOSIDE
ROBENZYLMERCAPTOPURINERIBORIERIBORIERIBORIERIBORIERIBORIERIBORIERIBORIERIBORIERIBORIERIBORIERIBORIERIBORIERIBORIERIBORIERIBORIERIBORIERIBORIERIBORIERIBORIERIBORIERIBORIERIBORIERIBORIER
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                                                                                                                                                                                                                                                            Score 123.8; DB 3; Length 1712; Pred. No. 2.3e-28; 0; Mismatches 32; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Version #1.30
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US-09-611-781-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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APPLICANT: Patel, Divyen
TITLE OF INVENTION: A NITR
TITLE OF INVENTION: (NBMCR
TITLE OF INVENTION: USE
TITLE OF INVENTION: USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "intron 2" HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 1341 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: April 9, 19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1712 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           646 GGCGTGAGCCACCGTGCCCAGCCTCATTCAACAAACTTTTAGTGTGCATCTACTG 700
                                                                                                         122 GGCATGAGCCACTGCGCCCAGCCGGTCTTTTTAAACATTCCCCAGGACTGTACAG 176
                                                                                                                                                                            586 GICTCGATCTCCTGACCTCGTGATCCTCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACA
                                                                                                                                                                                                                                                                                                              526 CGCGGCTATTTTTTTTTTTTTTAGTAGAGACGGGTTTTCACCGTGTTTAGCCAGGATG 585
                                                                                                                                                                                                                                                                                                                                                                                                                                               143;
                                                                                                                                                                                                                                           62 GTCTCGAACTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACA 121
                                                                                                                                                                                                                                                                                                                                                                      2 CGAGTTTTTTTTTTTTTTTTTTTTAAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATG 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A NITROBENZYLMERCAPTOPURINERIBOSIDE (NBMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSPORT PROTEIN, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.3%; Score 123.8; DB 4;
81.7%; Pred. No. 2.3e-28;
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Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1712;
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122 GGCATGAGCCACTGCGCCCAGCCGGTCTTTTTAAACATTCCCCAGGACTGTACAG 176

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US-09-058-389A-12

HYPOTHETICAL:

TOPOLOGY:

linear ö

STRANDEDNESS:

double

nucleic acid

ENGTH:

1712 base pairs

Query Match Matches

Local

Similarity

14.3%; 81.7%;

143; Conservative

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US-09-058-389A-5
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                                                                                                                          Sequence 5, Application US/09611781 Patent No. 6423829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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APPLICATION: April 9, 1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 5:
                                                                                  GENERAL INFORMATION:
APPLICANT: Belt,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLS OF INVENTION: A NITROBENZYLMERCAPTOPURINERIBOSIDE TRANSPORTITIES OF INVENTION: (NBMPR)-INSENSITIVE, EQUILLERATIVE, NUCLEOSIDE TRANSPORTITIES OF INVENTION: PROTEIN, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF TITLS OF INVENTION: USE
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
APPLICANT: Belt, Judith A.
APPLICANT: Crawford, Charles R.
APPLICANT: Patel, Divyen
TITLE OF INVENTION: A NITROBENZYLMERCAPTOPURINERIBOSIDE
TITLE OF INVENTION: (NEMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 411 Hackensack Ave, STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Focal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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                                                                                                                                                                                                                                                        1231 GGCGTGAGCCACCGTGCCCAGCCTCATTCAACAAACTTTTAGTGTGCATCTACTG 1285
                                                                                                                                                                                                                                                                                                                                           1171 GICTCGATCTCCTGACCTCGTGATCCTCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                 1111 CGCGGCTATTTTTTTTTTTTTTTTTAGTAGAGACGGGTTTTCACCGTGTTAGCCAGGATG 1170
                                                                                                                                                                                                                                                                                  122 GGCATGAGCCACTGCGCCCAGCCGGTCTTTTAAAACATTCCCCAGGACTGTACAG 176
                                                                                                                                                                                                                                                                                                                                                                     62 GTCTCGAACTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 CGAGTTTTTTTTTTTTTTTTTTTTTAAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATG 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
EDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6354 base pairs
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Crawford, Charles R.
Patel, Divyen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 123.8; DB 3; DB 3; Pred. No. 4.6e-28; Indels
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Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3; Length 6354;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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GENERAL INFORMATION:
APPLICANT: BEASLEY,
TITLS OF INVENTION:

BEASLEY, Ellen

ISOLATED HUMAN PHOSPHOLIPASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE

SOFTWARE:

LENGIH: 16063

CURRENT APPLICATION NUMBER: US/09/801,052 CURRENT FILING DATE: 2001-03-08 NUMBER OF SEQ ID NOS: 5

FastSEQ for Windows Version 4.0

FILE REFERENCE: TITLE OF INVENTION:

CL001045

PROTEINS, AND USES THEREOF

Sequence 3, Application US/09801052 Patent No. 6368842

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US-09-801-052-3/c
                   RESULT 9
                                                                                                                                                                                                                                                                                                                            Matches 143;
                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 6354 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION UDATA:
APPLICATION NUMBER: US 09
FILING DATE: April 9, 199
ATTORNEY/ACENT INFORMATION:
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPB: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-013N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 411 Hackensack Ave, Continental Plaza, STREET: Floor
                                                                                                                                                                                                                                                                                                                                                Match 14.3%; Score 123.8; DB 4; Length 6354; Local Similarity 81.7%; Pred. No. 4.6e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/611,781
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                                                                               1231 GGCGTGAGCCACCGTGCCCAGCCTCATTCAACAAACTTTTAGTGTGCATCTACTG 1285
                                                                                                                                                              1171 GECTEGATETECTGACCTEGTGATECTCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACA
                                                                                                                                                                                                                                             1111 CGCGGCTATTTTTTTTTTTTTTTAGTAGAGACGGGTTTCACCGTGTTAGCCAGGATG 1170
                                                                                                                    122 GGCATGAGCCACTGCGCCCAGCCGGTCTTTTTAAACATTCCCCCAGGACTGTACAG 176
                                                                                                                                                                                          62 GTCTCGAACTCCTGACCTCGTGATCCGCCCCGCCTCGGCCTCCCAAAGTGCTGGGGATTACA 121
                                                                                                                                                                                                                                                                                       2 CGAGTTTTTTTTTTTTTTTTTTAAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATG
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                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA (genomic)
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                                                                                                                                                                                                                                                                                                                              0; Mismatches
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RESULT 11
US-08-330-272-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: BEASLEY, Ellen et al.
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
                                                                                                                                 Sequence 5, Application Patent No. 5985598 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Patent No. 6638747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/020,121
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US 60/255,386
PRIOR FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: US 09/801,052
PRIOR APPLICATION NUMBER: US 09/801,052
PRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 5
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: CL001045DIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 16063
                                       TITLE OF INVENTION: TCL-1 Gene and Protein and Related TITLE OF INVENTION: Methods and Compositions NUMBER OF SEQUENCES: 11
                      CORRESPONDENCE ADDRESS
                                                                                                           APPLICANT:
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Local Similarity 93.5%;
  ADDRESSEE:
                                                                                                                                                                                                                                                                                                   102
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                                                                                                                                                                                                                                                                                                                                               128 AGCCACTGCGCCCAGCCG 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 TETTITITITITITITAAGIAGAGATGGGGTTTCACCGTGTTAGCCAGGATGGTCTCG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 TITTITITITITITITAAGTAGAGAIGGGGITICACCGIGITAGCCAGGAIGGICICG 67
                                                                                                                                                                                                                                                                                                   AGCCACCGCGCCCAGCCG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTTTTTTTTGTATTTTTAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATGGTCTCG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                   AACTECTGACCTCGTGATCCGCCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATG 127
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                                                                                                                                                                                  Application US/08330272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                              Russo et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.3%; Score 123.6; DB 4; Length 16063; 93.5%; Pred. No. 8.8e-28;
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Pred. No. 8.8e-28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Indels
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SOPTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/13663

ATTORNEY/AGENT INFORMATION:

CATION:

CLASSIFICATI

COMPUTER READABLE FORM:

COUNTRY: STATE:

U.S.A.

New York

10036

MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

APPLICANT: Russo et al TITLE OF INVENTION: TCL-1 Gene and Protein and Related TITLE OF INVENTION: Methods and Compositions

NUMBER OF SEQUENCES: 1

STREET: 1155 A

1155 Avenue of the Americas

Pennie & Edmonds

ADDRESSEE:

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WOLECULE TYPE:
US-08-330-272-5
                                    RESULT 12
PCT-US95-13663-5
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Sequence 5, Application PC/TUS9513663 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1155 Aver
CITY: New York
STATE: New York
COUNTRY: U.S.A.
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/330,272
                                                                                                                                                                                                                                                                                                                                                                                                 Match 14.2%; Score 123; DB 2; Length 4922; Local Similarity 85.2%; Pred. No. 7.1e-28;
                                                                                                                           3411 TGAGCCACCACGTCCGGCCTTACCATTGCTTTATT 3445
                                                                                                                                                                                                          3351 CGATCTCCTGACCTCATGATCTGCCCGGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCA 3410
                                                                                                                                                                                                                                                                                             3291 Tritrititititititititititititakiakimoseserititakoosisitiaksooaksalisitot 3350
                                                                                                                                                                  126 TGAGCCACTGCGCCCAGCCGGTCTTTTTAAACATT 160
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                                                                                                                                                                                                                                                                                                                                    6 TITTITTTTTTTTTTTTTAAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATGGTCT 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (212) 790-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               530
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    Mismatches

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REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6754-027
TELECOMMUNICATION INFORMATION:

TELEPHONE:

NAME: Misrock, S. Leslie REGISTRATION NUMBER: 18,

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                                                                                                                                                                                                                                             Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.0 SEQ ID NO 38 LENGTH: 128779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 38, Application US/09497855A Patent No. 6605432
                                                                                                                                                                                                                             Matches 129;
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                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/497,855A CURRENT FILING DATE: 2000-02-04 PRIOR APPLICATION NUMBER: 60/120,592 PRIOR FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: 60/118,760 PRIOR APPLICATION NUMBER: 60/118,760 PRIOR FILING DATE: 1999-02-05 UNMBER OF SEQ ID NOS: 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Huang, Tim
TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
FILE REFERENCE: UMO1523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212) 790-8864/9:
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                  17434 TTTTTTTTTTTTGTATTTTÄĞİÄĞAGACGGGGTTTCACCATGTTÄĞCCÄGĞATGGTCT 17375
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17314 TGAGCCACTGTGCCCGGCC 17296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3291 TITTTTTTWTTWTTTTTTAGTAGAGMCGGGGTTTCACCGTGTTAGCCAGGATGGTCT 3350
                                  126
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                                                                                                               66 CGAACTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCA 125
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                                                                         CGATCTCCTGACCTCGTGATCCGCCCGACTCGGCCTCCCAAAGTGCTGGGATTACAGGCG 17315
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(212) 790-8864/9741
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                                                                                                                                                                                                                                           Score 123; DB 4; Length 128779; Pred. No. 4.2e-27;
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RESULT 14

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; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Mario
; TITLE OF INVENTION: ISOLA
; TITLE OF INVENTION: THER
; FILE REFERENCE: CL001164
                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: WEBSTER, MARION et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PR
TITLE OF INVENTION: ACID MOLECULES ENCODING
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO1164ADIV
CURRENT APPLICATION UNMBER: US/10/238,709
CURRENT FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-804-471A-3/c
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                                                                                                                        Matches 132;
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Patent No. 6680188
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LENGTH: 174493
TYPE: DNA
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                                                                                                                                                                  Query Match
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Best Local Similarity
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CURRENT FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                          PEATURE: FEATURE LOCATION: (1)...(174493)
OTHER INFORMATION: n = A,T,C or G
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NAME/KEY: misc_feature
LOCATION: (1)...(17449
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                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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                                                                                                                                          Match 14.1%; Score 122.4; DB 4; Length 174493; Local Similarity 89.2%; Pred. No. 7.6e-27;
                                     88881
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66 CGAACTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCA 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marion et al
ISOLATED HUMAN KINASE PROTEINS, NUCLBIC
ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAXION et al
ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
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Db 88941 CGATCTCCTGACCTCATGATCTGCCCCCCTCAGCCTCCCAAAGTGCTGGGATTACAGGGG B8882

Qy 126 TGAGCCACTGCGCCCAGCCGGTCTTTT 153

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Search completed: May 24, 2004, 15:50:37

Job time: 74 secs

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                                                                                                                    Query
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Copyright (c) 1993 - 2004 Compugen Ltd.
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CA392561
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CA392561 C826b04.y
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CA866165 ir39a06.x
AW193512 xm17b12.x
                                                                                                   Description
                                                                                JOURNAL
MEDLINE
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COMMENT
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ORGANISM
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1 (bases 1 to 586)

Wistow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A.,

Wistow,G., W., Bouffard,G., Smith,D. and Peterson,K.

Expressed sequence tag analysis of human RPE/choroid for the

EXPRESSED SEQUENCE TOVER 6000 non-redundant transcripts, novel genes
                                                                                                                                                                                                                                                                                                                                                                                                                                    CA392561

CB26b04.yl Human Retinal pigment epithelium/choroid cDNA
(Un-normalized, unampilfied): cs Homo sapiens cDNA clone cs26b04
                   Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
                                                                                Contact: Wistow G
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                   12107410
                                                                                                                                        and splice variants
Mol. Vis. 8 (4), 205-220 (2002)
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BE675952 7d49b07 x
AU148124 AU148124
AQ123954 HS 3103 A
BX641257 DXFZp666F
CB055059 VISC 2007
AG011645 Homo Sapi
AQ893423 HS 3148 A
BG675124 602621392
BQ436628 AGENCOURT
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AI521901 ti80d03.x
AI493546 th36b01.x
AQ387243 RPCI11-15
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CD171998 AGENCOURT
BUG19183 UI-H-FH1-
BC041578 Homo sapi
AA7264969 xq58f07.x
BUG38849 AGENCOURT
BQ681574 AGENCOURT
BQ681574 AGENCOURT
BQ681574 AGENCOURT
BUG29053 UI-H-FL0-
AG150406 Pan trog1
BX475938 DKFZp686G
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AV738722 AV738722
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Plate: 26 row: b column:
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AGTCCAAACAGGCCCAAATGCATTCATGAGCAGGGGGAGGCCAAAGGACTCCGGAGGAGA 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="Numan Retinal pigment epithelium/choroid cDNA (Un-normalized, unamplified): cs"
/mote="Organ: Eye; Vector: pcMVSPRT6; Two different donor eyes (T5-80 years old) yielded approximately 600 mg of dissected RPB/choroid tissue. This in turn yielded 340 ug of total RNA and 7 ug of mRNA. A directionally cloned cDNA library in the pcWVSPDRT6 vector was constructed at Life Technologies (Rockville, MD; now part of Invitrogen CDP), essentially following the protocols of the SuperScript plasmid System (Invitrogen COTP).
chttp://www.invitrogen.com/>). The library code designation was cs. For this library, cDNA inserts were cloned into the NotI/Mul sites of the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
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/dev_stage="Adult"
/lab_host="EMDH10B"
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Query Match
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C526b05.yl Human Retinal pigment epithelium/choroid cDNA
(Un-normalized, unamplified): cs Homo sapiens cDNA clone cs26b05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
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Plate: 26 row: b column: 05
Seg primer: M13RP1 reverse primer (ABI).
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Fax: 301 496 0078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                 Similarity
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                                                                                                                  Conservative
                                                                                                                                                                                                                                                  /clone lib="Human Retinal pigment epithelium/choroid cDNA (Un-normalized, unamplified): cs"
/mote="Organ: Eye; Vector: pcMVSPORT6; Two different donor eyes (75-80 years old) yielded approximately 600 mg of dissected RPE/choroid tissue. This in turn yielded 340 ug of total RNA and 7 ug of mRNA. A directionally cloned cDNA library in the pcMVSPORT6 vector was constructed at Life Technologies (Rockville, MD; now part of Invitrogen Corp), essentially following the protocols of the SuperScript plasmid System (Invitrogen.com/>). The library code designation was cs. For this library, cDNA inserts were cloned into the Notl/Mul sites of the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="Adult"
/lab_host="EMDH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="RPE/choroid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="cs26b05"
                                                                                                                                              99.3%;

    Mismatches

                                                                                                                                              Score 560; DB 1.
Pred. No. 4e-96;
                                                                                                                                                                          DB 14; Length 586;
                                                                                                                            Gaps
            527
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TCTTTTAAACATTCCCCAGGACTGTACAGCCAACCCATACTCACCTGACATTTGGGAAC

206

CGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCCAGCCGG 146

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REFERENCE
AUTHORS
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CA866165
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                                                                                                                                                                                                                 Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
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Kelton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Leenishka, I., Scearce, M., Bresteili, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, B., Ronko, I., Bennett, J., Schmitt, A., Theising, B., Ritter, B., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endocrine Pancreas Consortium
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                                                                                                                                                                                                                                                                                                                                               Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
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                                                                                                                                                                                               primer: -40RP from Gibco
                                                                                                                                             quality sequence stop: 450.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                 of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                         617-495-1812
                    /organism="Homo sapiens"
/moi_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6547308"
/tissue_type="Purified pancreatic islet"
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                                                                                                                                                                                     TACTGGGCGA-GCTGCCACCTGCTACAGTGAAGGGATCTGGAGAAATACTCACACTTTG
                                                                                                                                                                                                                                                                                     TCTAGGTCTTTCTTACCACAAACACCTCTCTGCCCACCTGCTTTGAAAGGGGCAGAAGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAACTCCCCCCACGGCCATAACTGATCTGCAGAGGTAAGACCAAGAGCAAGAATGGGG
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                                                                                AGGTGCTCGCCCTCTTCATCAGCCAGCTCTAACTTAAGCCAATGACCCCACGGGAGCCTT
                                                                                                                     AGGTGCTCGCCCTCTTCATCAGCCAGCTCTAACTTAAGCCAATGACCCCACGGGAG-CTT
                                                                                                                                                                                                                                                TCTAGGTCTTTCTTACCACAAACACCTCTCTGCCCACCTGCTTTGAAAAGGGGCAGAAGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="DH10B"
/clone lib="HR85 islet"
/clone lib="HR85 islet"
/clone lib="HR85 islet"
/note="Torgan: Panoreas; Vector: pBluescript SK(-); Site_1:
/note: Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size -1kb. 5'
XhoI site was destroyed after directional cloning.
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, ND,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@amgate.wustl.edu, Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                314-362-1916, Fax: 314-747-2692."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.0%;
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Pred. No. 3e-85;
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REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                  xm17b12.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2684447 3
similar to contains Alu repetitive element;contains element HGR
repetitive element;, mRNA sequence.
                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 491)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
               Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg,
                                                                                                                                                                   Homo sapiens
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EST 29-NOV-1999

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FEATURES
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cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 395.
AGENCOURT_8484953 NIH_MGC_113
5', mRNA sequence.
                                                                      BQ710765
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall;
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Noti; Cloned unidirectionally. Primer: Oligo dT.
Site_2: noti; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.48 kb. Life Technologies catalog #:
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/mcl_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2684447"
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                      941 bp mRNA ilnear soi is vous 2002-2002 and clone IMAGS:6301113
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       801 GGCTCCTCAAGGTCAGCTGTGGCCTTGANTGAAYCACCTGCTATGACCAAT 853
                                                                                                                                                                                                                413 AGAATGAGCAGGACTAACACCTGGGTGTCATGGCAAGCCTCCAGGGGCCGACTGGCCAGAG
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MCC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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1 (bases 1 to 941)
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/clone lib="NIH MGC_113"
/clone="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
/corgi; cDNA made by oligo-dT priming. Directionally cloned into EccRI/XhoI sites using the following 5' adaptor:
/corgix GCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California,
/erkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI521901 421 bp mRNA linear EST 13-APR-1999 ti80d03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138309 3' similar to contains Alu repetitive element;contains element PTR5
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Location/Qualifiers
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prepared, and so circles were made in vitro: Following Hab purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 132376-1323911, 1456007-1456775, and IS00552-1502855). Subtraction by Bento Soares and M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:2138309"
/lab host="H108"
/clone_lib="NCI_CGAP_Kid11"
/clone_lib="NCI_CGAP_Kid11"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; plasmid DNA from the normalized library NCI_CGAP_Kid3 was plasmid DNA from the normalized library 
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Insert Length: 882 Std Error: 0.00
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392 bp mRNA linear EST 30-MAR-1999 th36b01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2120329 3' similar to contains Alu repetitive element; mRNA sequence.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTAGGTCTTTCTTACCACAAACACCTCTCTGCCCACCTGCTTTGAAAGGGGCAGAAGTA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATTCACATCTAAGGTCTGGTGATGGCTGATGAAGGAAGAAGAATCAGCGAACAAAAGCC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTAGGTCTTTCTTACCACAAACACCTCTCTGCCCACCTGCTTTGAAAGGGGCCAGAAGTA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Technologies catalog #: 11548-013
                                                                                                                                                                                                                      TTTTTTTTTTTTTTTAAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATGGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: Sall; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.72 kb. Life Technologies catalog #:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone_lib="NCI_CGAP_Pan1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue_type="adenocarcinoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     th: 882 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                Score 253; DB 9;
Pred. No. 5.6e-38;
                                                                                                                                                                                                                                                                                                                                                                        Length 392;
                                                                                                                                                                                                                                                                                                       Indels
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259
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RESULT 8 AQ387243

DEFINITION

KEYWORDS VERSION ACCESSION

ORGANISM

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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 ACTCACCTGACATTTGGGAACTCCCCCCCACGGCCATAACTGATCTGCAGAGGTAAGACC 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 TGAGCCACTGCGCCCAGCCGGTCTTTTAAACATTCCCCCAGGACTGTACAGCCAACCCAT 185
                                                                                                                                                                                                         139;
                                                                  99
                                                                                                              27
                                                                                                                                                       σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Other GSSs: RPCI11-154N12.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter, J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 574)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPCI11-154N12.TV RPCI-11 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: hbe@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ387243.1 GI:4358266
                 CGATCTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAATGCTGGGATTACAGGCG 146
                                                   CGAACTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGAGCAAGAATG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTCACCTGACATTTGGGAACTCCCCCCCACGGCCATAACTGATCTGCAGAGGTAAGACC 379
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301 838 0208
                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens
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                                                                                                                                                                                                                                                                                                                  /cell_type="1ymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/RPCI11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="GDB:7559075"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                  sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="RPCI-11-154N12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
                                                                                                                                                                                                                          93.98;
                                                                                                                                                          TITTTTTAAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATGGTCT 65
                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                          Score 133.6; DB 28; Pred. No. 1.8e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens genomic clone RPCI-11-154N12,
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                                              DEFINITION
                                                                                                                RESULT 10
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  ACCESSION
                                                                                          AQ423092/c
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BX504260/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
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                                                                                                                                                                                                                               122 GGCATGAGCCACT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 TGAGCCACTGCGCCCAGCCGGTCTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           132;
                                                                                                                                                                                                                                                                                                                       62
                                                                                                                                                                                     16
                                                                                                                                                                                                                                                                             76
                                         AQ423092 590 bp DNA linear GSS 23-MAR-1
CITBI-E1-2575M23.TR CITBI-E1 Homo sapiens genomic cione 2575M23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by DKFZ (German Cancer Research Center,
AQ423092
                      genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berlin-Charlottenburg, GERMAN
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST (Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R., et al.)
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BX504260
615 bp mRNA linear EST 04-SEP DKFZp686E20133_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone DKFZp686E20133 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Please contact the RZPD: Ressourcenzentrum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone (DKFZp686E20133) is available at the RZPD in Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No si sequence available.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mewes, H.W., Weil, B., Amid, C., Osanger, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Poustka, A., Albert, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wiemann,S.
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                                                                                                                                                                                     GGCATGAGCCACT 4
                                                                                                                                                                                                                                                                                                                            GTCTCGAACTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACA 121
                                                                                                                                                                                                                                                                                                                                                                     CGATTTTTTTTTTTTTTTTTTAAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="DKF2p686E20133"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="686 (synonym: hlcc3)"
/note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.2%;
99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                               TTTTTTTTTAAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 131.4; DB 1
Pred. No. 4.6e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moosmayer,P., Schupp,I., Wellenreuther unid.C., Osanger,A., Fobo,G., Han,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GERMANY; Email: clone@rzpd.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                       GSS 23-MAR-1999
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COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364 ATTTTTTTTTTTTTTTTTTAGTAGAGACGGGGTTCACCTTGTTAGCCAGGATGGT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 CATGAGCCACTGCGCCCAGCC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 CTCGAACTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 AGTITITITITITITITITITAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATGGT 63
                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 599)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
                                       discovery
                                                                                                                                                                                                                                                                                BU689261 699 bp mRNA linear BST 07-0
UI-CF-EC1-adw-o-18-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
UI-CF-EC1-adw-o-18-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
  97044477
                    Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                            Homo sapiens (human)
                                                              Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                           BU689261.1 GI:23546857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9712 Medical Center Dr., Rockville, MD 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Other_GSSs: CITBI-E1-2575M23.TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter, J.C.
Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhao,S., Adams,M.D., Nierman,W., Malex,J., Shizuya,H., Simon,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ423092.1 GI:4480B16 GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     CATGAGCCACTGCGCCCGGCC 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTGATCTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 590)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_type="sperm"
/clone_lib="CITBI-E1"
/clone_vertor: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
CalTech Human BAC Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="2575M23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sex="male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (1997)
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Pred. No. 9.5e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                              EST 07-OCT-2002
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RESULT 12 AA599141 LOCUS DEFINITION

AA599141 292 bp mRNA linear EST 06-MAR-1998 ae52d02.sl Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:950499 3' similar to contains Alu repetitive element;contains

element MER40 repetitive element ;, mRNA sequence.

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                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                      Local Similarity
121
                                                                                                                                                                                                                                                                                                                         132;
                                                       128 AGCCACTGCGCCCAGCC 144
                                                                                                               13
                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: M13 FORWARD POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (www.openbiosystems.com).
The following repetitive elements were found in this cDNA
sequence: 7-137, >ALU (matched compliment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 319 356 4866
Fax: 319 356 7171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8889548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetics (www.resgen.com) or from Open Biosystems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: McCray, PB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McCray Lab
                                                                                                            ATCTCCTGACCTCGTGATCTGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATG
                                                                                                                                               AACTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATG 127
                                                                                                                                                                                                                                                                    TITTTTTTTTTTTTTTTTAAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATGGTCTCG
                                                                                                                                                                                                                        TTTTTTTTTTTTTTTCAGTAGAGACGGGGTTTCACCGTGTTAGCCAGGATGGTCTCG
  AGCCACTGCACCCAGCC 137
                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /notes—Torgan: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-CF-ECI is a normalized-CDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Leannon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime sequence that is located between the Not I site and the [dT]18 tail. The sequence tag for this library is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAG_LIB=UI-CF-EC1
TAG_SEQ=AAGTGCTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev stage="Adult and Fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone lib="UI-CF-EC1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/clone="UI-CF-EC1-adw-o-18-0-UI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ=AAGTGCTTAC"
                                                                                                                                                                                                                                                                                                                                                      14.9%;
96.4%;
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                                                                                                                                                                                                                                                                                                                                                      Score 129; DB 13;
Pred. No. 1.3e-14;
                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   Length 699;
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COMMENT
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                                            VERSION
KEYWORDS
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    SOURCE
                                                                                                                                                                                                          DEFINITION
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                                                                                                                                                                                                                                                                                                                                          RESULT 13
                                                                                                                               ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 CGAACTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TGATCTCCTGACCTCGTGATCCACCCACCTCGGCCTCCCAAAGCGCTGGGATTCCAGGTG 120
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                                                                                                                  S07 bp mRNA linear ES:
AGENCOURT 14065742 NIH MGC_181 Homo sapiens cDNA clone
IMAGE:30375733 5', mRNA sequence.
CD171998
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Seg primer: -40m13 fwd. BT from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
Homo sapiens (human)
                                                                                        CD171998.1 GI:30853082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTIGICT 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rdadecachdereceadecerrectiticaaerarretrecteaerecarrecageree 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTCACCT 193
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314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_Stage="cell line NCI-H69"
/lab host="SOLR (kanamycin resistant)"
/lab host="SOLR (kanamycin resistant)"
/clone lib="Stratagene lung carcinoma 937218"
/clone lib="Stratagene lung carcinoma 937218"
/cloned inung strate lung strate lung carcinoma en lung strate libe lung carcinoma en lung strate libe lung strate libe lung strate lung strate libe lung strate lung
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/cell_line="NCI-H69"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:950499"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.9%; Score 128.8; DB 9; Length 292; BD.3%; Pred. No. 2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37;
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COMMENT
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TITLE
                                                                                                                                                 AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
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                                                                                                                                                                                                                                                                        ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               445 CTCTTGACCTCGTGATCCACCCGTCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAG 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 507)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 507.
Tumor Gene Index (Ingor) (1997) (Ingublished (1997) (Ingublished (1997) (Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 647)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                          BU619183 647 bp mRNA linear EST 23-SEP UI-H-FH1-bfn-k-19-0-UI.s1 NCI_CGAP_FH1 Homo sapiens cDNA clone UI-H-FH1-bfn-k-19-0-UI 3', mRNA sequence.
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Plate: NDAM437 row: d column: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                BU619183.1 GI:23285398
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CDNA Library Arrayed by: The I.M.A.G. E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTTTTTTTTTTTTTTAGTAGAGACGGGGTTTCACCGTGTTAGCCAGGATGGTCTCGAA 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="White Matter"
/dev_stage="Unknown"
/lab_host="DH108-Ton A ( T1 and T5 phage resistances) "
/clone_lib="NIH_MCC_181"
/clone_lib="NIH_MCC_181"
/clone_tib="NIH_MCC_181"
/destroyed); Library is oligo-df primed and directionally cloned (BcoRV site is destroyed upon cloning). Average insert size 1.42 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC_Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type="mRNA"
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Pred. No. 1.7e-14;
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REFERENCE
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ORGANISM
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                                                                                                                                                                                                                                                                                  KEYWORDS
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                                                                            AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GCCACCACGCCAGCCACCAGTTTTAAAAAT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 GCCACTGCGCCCAGCCGGTCTTTTAAACAT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TCTCCTGACCTCGTGATCTGCCCGGCCTCGGCCTCCCAAAGTGCTGGGACTACAGGCGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 ACTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGA 128
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3538)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Colline,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 TITITITITITITAGZAGAGATGGGGTITCACCGTGTTAGCCAGGATGGTCTCGA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu

The following repetitive elements were found in this cDNA sequence: 6-136, >ALU (matched compliment)

Seq primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                               BC041578 sapiens hypothetical protein MGC17986, mRNA (cDNA clone
                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                 Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                   BC041578.1 GI:27469657
                                                                                                                                                                                                                                                                                                                                                                                     IMAGE: 4640152), with apparent retained intron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLYA=Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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//clone Torgan: Chondrosarcoma, Vector: pT7T3-Pac
/note="Torgan: Chondrosarcoma, Vector: pT7T3-Pac
(Pharmacia) with a modified polylinker; Site 1: BcoR I;
Site 2: Not I; NCI CGAP FH1 is a normalized cDNA library
obtained from a cell line derived from grade I
chondrosarcoma tissue. The library was constructed and
normalized according to Bonaldo, Lennon and Soares, Genome
Research, 6:791-806, 1996. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EcoR I adaptor,
digested with Not I, and cloned directionally into
pT7T3-Pac vector. The oligonucleotide used to prime the
synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
AGAATCCGGC. The cell line was provided by Dr. James Martin
from the University of Iowa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAG_SEQ=AGAATCCGGC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="UI-H-FH1-bfn-k-19-0-UI"
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S

片 Ś ₽ Ś B

문 Ś ORIGIN

Matches 134; Query Match

Conservative

9 TTTTTTTTTTTTTAAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATGGTCTCGA 68

TITTTTTTTTTTTTTTAGTAGAGACGGGGTATCACCGTGTTAGCCAGGATGGTCTTGA 2163

Local Similarity

14.8%; 93.7%;

Score 128.6; DB 11; Pred. No. 7.5e-15; Mismatches

Length 3538;

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PEATURES
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                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLML at: http://image.llnl.gov Series; IRAL Plate: 44 Row: e Column: 10

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23957699

This clone has the following problem: retained intron.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: nisc_mgc@nhgri.nih.gov

Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

Blakkesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,

Blatkesley,R.W., Bouffard,G.G., Breen,K., Gupta,J., Haghighi,P.,

Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,

Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,

Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,

McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,

Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,

Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (20-DEC-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Co.
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Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                                        /clone="IMAGE:4640152"
/tissue type="Skin, melanotic melanoma."
/clone_Tib="NIH_MGC_20"
/lab_host="DH10B-R"
                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
'note="Vector: pOTB7"
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COMMENT

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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ACCESSION VERSION RESULT 1 AW193512 COMMENT REFERENCE SOURCE KEYWORDS DEFINITION LOCUS JOURNAL TITLE ORGANISM AUTHORS AW193512 491 bp mRNA linear EST 29-NOV-1999 xm17b12.x1 NCI CGAP Ut4 Homo sapiens cDNA clone IMAGE:2684447 3' similar to contains Alu repetitive element;contains element HGR repetitive element;, mRNA sequence. Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 491)
MCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP language Institute, Cancer Genome Anatomy Project (CGAP); Unpublished (1997) Homo sapiens Homo sapiens (human) AW193512.1 GI:6472211

cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Greg Lemon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CCAP clone distribution information can be cound through the I.M.A.G.B. Consortium/LLNL at:

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REFERENCE
AUTHORS
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High quality sequence stop: 395.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
                                          Contact: Robert Strausberg, Ph.D.
                                                          Unpublished (1997)
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/db_xref="taxon:9606"
/clone="IMAGE:2684447"
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                                                                                                                                                                                                                                                                          GI:4436036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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SOURCE

ORGANISM

Homo sapiens

Homo sapiens

(human)

DEFINITION
ACCESSION
VERSION
KEYWORDS

EST

CA866165.1 GI:27317714

CA866165

mRNA sequence

ir39a06.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6547308

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                   CA866165
POCUS
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cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image/html

Insert Length: 718 Std Error: 0.00
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CA866165
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                                                                                                                                                           TAGTGGGCGAG 392
                                                                                                                                                                                                       TCTAGGTCTTTCTTACCACAAACACCTCTCTGCCCACCTGCTTTGAAAGGGGGCAGAAGTA
                                                                                                                                                                                                                                                                                                                                            GATTCACATCTAAGGTCTGGTGATGGCTGATGAAGGAAGAAGAATCAGCGAACAAAAGCC 321
                                                                                                                                                                                                                                                                                                                                                                                        GGAACTCCCCCCACGGCCATAACTGATCTGCAGAGGTAAGACCAAGAGCAAGAATGGGG
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                                                                                                                                                                                                                                                                                                  GATTCACATCTAAGGTCTGGTGATGGCTGATGAAGGAAGAAGAATCAGCGAACAAAAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="NCI CGAP_Kid11"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
plasmid DNA from the normalized library NCI_CGAP_Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo. "
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/db_xref="taxon:9606"
/clone="IMAGE:2138309"
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  527 bp
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 TGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCCA 141
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1 (bases 1 to 527)

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Mylle,T., Marrin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,B., Ronko,I., Benett,J., Schmitt,A., Theising,B., McCann,R., Cole,R., Tsagareishvili,R., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Mylliams,T., Jackson,Y. and Bowers,Y.
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Location/Qualifiers
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Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
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                                                                                                                                                                  GATTCACATCTAAGGTCTGGTGATGGCTGATGAAGGAAGAATCAGCGAACAAAAGCC 300
                                                                                              TCTAGGTCTTTCTTACCACAAACACCTCTCTGCCCACCTGCTTTGAAAGGGGCAGAAGTA 381
                                                                                                                                                                                                                                                                                                               GGAACTÓCCCCCACGGCCATAACTGATCTGCAGAGGTAAGACCAAGAGCAAGAATGGGG 240
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                                                                                                                                                                                                                                   GATTCACATCTAAGGTCTGGTGATGGCTGATGAAGGAAGAAGAATCAGCGAACAAAAGCC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCGGTCTTTTTAAACATTCCCCAGGACTGTACAGCCAACCCATACTCACCTGACATTTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCCA 1:20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        617-495-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size -1kb. 5' XhoI site was destroyed after directional cloning. Amplified once: Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Pax: 314-747-2692."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:6547308"
/tissue_type="Purified pancreatic islet"
/lab_host="DH108"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.8%; Score 371; DB 14; 100.0%; Pred. No. 1.1e-52;
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ORGANISM
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1 (bases 1 to 586)
Wistow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A., Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.

Expressed sequence tag analysis of human RPE/choroid for the Millank Project: Over 6000 non-redundant transcripts, novel genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: graeme@hellx.nih.gov
Plate: 26 row: b column: 04
Seg primer: M13RP1_reverse primer (ABI).
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/dev_stage="Adult"
/lab_host="BMDH10B"
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/db_xref="taxon:9606"
/clone="cs26b04"
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CA392562

CS26b05.yl Human Retinal pigment epithellum/choroid cDNA

(Un-normalized, unamplified): cs Homo sapiens cDNA clone cs26b05
                                                                                                                                                                                                                                                                                                                                            Email: graeme@helix.nih.gov
Plate: 26 row: b column: 05
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wistow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A., Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
Expressed sequence tag analysis of human RPB/choroid for the NEIBank Project: Over 6000 non-redundant transcripts, novel genes
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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essentially following the protocols of the SuperScript plasmid System (Invitrogen Corp. <a href="http://www.invitrogen.com/">http://www.invitrogen.com/</a>). The library code
                                                    /note="Organ: Eye; Vector: pCMVSPORT6; Two different donor eyes (75-80 years old) yielded approximately 600 mg of dissected RPE/choroid tissue. This in turn yielded 340 ug of total RNA and 7 ug of mRNA. A directionally cloned cDNA library in the pCMVSPORT6 vector was constructed at Life Technologies (Rockville, MD; now part of Invitrogen Corp).
                                                                                                                                                              /clone lib="Human Retinal pigment epithelium/choroid cDNA (Un-normalized, unamplified): cs"
                                                                                                                                                                                                   /dev_stage="Adult"
/lab_host="EMDH108"
                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.2%; Score 366; DB 14;
100.0%; Pred. No. 6.7e-52.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 941)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5', mRNA sequence.
BQ710765
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AGENCOURT_8484953 NIH_MGC_113
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                                                                                                                                                                                              quality sequence stop:
/organism="Homo sapiens"
/mol type="mRNA"
/db Xref="taxon:9606"
/clone="IMAGE:6301113"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                    Location/Qualifiers
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C 113 Homo
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ORIGIN

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FEATURES
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        525 CCCAATAAGGCTGGCGCTATTTCCGATCCATAGAGAGAGCAGAGGTGGGCAGGCCCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                585 CAAACAGGCCCAAATGCATTCATGAGCAGGGGGGGGGCCAAAGGACTCCGGAGGAGAGAGGG 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              509 CAAACAGGCCCAAATGCATTCATGAGCAGGGGGAGGGCCAAAGGACTCCGGAGGAAGAGG 568
                                                                                                                     Insert Length: 882 Std Error: Seq primer: -40UP from Gibco
High quality sequence stop: 391.
Location/Qualifiers
                                                                                                                                                                                             Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NAI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 882 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.mih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI493546
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392 bp mRNA linear EST 30-MAR-1999 th36b01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2120329 3' similar to contains Alu repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE;2120329"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.38;
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                                                                                                                                                                                                                                                                                                                      Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Email s.wiemann@dkfz- heidelberg.de; sequenced by DKF2 (German Cancer Research Center, Berguenced by DKF2 (German Cancer Research Center, Berguenced by DKF2 (German Cancer Research Center, Berguenced by DKF2 (German) within the cDNA sequencing consortium of the
                                                                                                                                                            Berlin-Charlottenburg, GERMA
Location/Qualifiers
                                                                                                                                                                                         This clone (DKFZp686B20133) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 615)

Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wicces, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BX504260

615 bp mRNA linear EST 04-SEP
DKFZp686E20133_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZp686E20133_5', mRNA sequence.
                                                                                                                                                                                                                                                                                                     German Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wellenreuther, R., Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST (Poustka, A., Albert, R., Moosmayer, P., Schupp, I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wiemann, S.
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                                                                                                                                                                                                                                                                             No si sequence available.
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/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Sal1;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKPZp686E20133"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="adenocarcinoma"
/lab_host="DH10B"
                                                                                                              organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                et al.)
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RESULT 9
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 TTTTTTTTTTTTTTTTTAAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATGGTCT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     507 bp mRNA linear EST 18-FEB-1998 no81h09.81 NCI CGAP AA1 Homo sapiens cDNA clone IMAGE:1113281 3' similar to gb.M80651 Hum ORF (HUMAN);contains Alu repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 CGAACTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 CGAACTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCA 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 507)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NALIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp//image/image.html
Insert Length: 1887 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: Cgapbs remail.nih.gov
Tissue Procurement: L. deffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 100.0%; P
                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA613893.1 GI:2466027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Stratagene, Inc., David B. Krizman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Arraying: Greg Lennon, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTTTTTTTTTTTTTTAAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATGGTCT 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens (human)
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/note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"
                                             /tissue_type="adrenal adenoma"
/tissue_type="adrenal adenoma"
/lab host="SOLR (kanamycin resistant)"
/clone_lib="NCI GAP AAl"
/clone_tib="NCI GAP AAl"
/note="Organ: adrenal gland; Vector: Bluescript SK-;
/site_1: EcoRI, Site_2: XhoI; Cloned unidirectionally.
Primer: Oligo dT. Two pooled bulk adrenal adenomas. 5'
adaptor sequence: 5' GAATTCGGCAGAG 3' 3' adaptor
sequence: 5', CTCGAGTTTTTTTTTTTTTTTTT 3' Average insert
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                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
/clone="IMAGE:1113281"
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                               1.6 kb."
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Query Match

8.8%

Score 76;

DB

9

Length 507;

VERSION KEYWORDS DEFINITION ACCESSION

POCUS

AV718792 592 bp mRNA linear EST 16-OCT-2 AV718792 GLC Homo sapiens cDNA clone GLCCOE12 5', mRNA sequence. AV718792

EST 16-OCT-2000

SOURCE

Homo sapiens (human) AV718792.1 GI:10815944

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RESULT 10
AV719687
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RESULT 11
AV718792
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                                                                                276 AGCCACTGCGCCCAGC 291
                                                                                                                         128 AGCCACTGCGCCCAGC 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qian,B., Wu,T., Huang,Q., Huang,C., Kang,B., Gao,X., Xu,Z., Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng, Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang,Y., Gu,Y., Chen,Z. and Han,Z. Homo sapiens cDNA GLC clones
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AV719687 GLC Homo sapiens cDNA clone GLCCBE07 5', mRNA sequence.
AV719687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76; Conservative
                                                                                                                                                                                                                                            76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GLCCBE07"
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                                                                                                                                                                                                                                                                                                                                                                 /note=#Vector: pBluescript sk(-); Site_1: EcoRI; Site
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                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue_type="corresponding non cancerous liver tissue"
                                                                                                                                                                                                                                                                                                                                                                                                          'lab host="SOLR"
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100.0%; Pred. No. 0.00039;
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                                                                                                                                                                                                                                                                                                                                                                                      lib="GLC"
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AV719326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 AGCCACTGCGCCCAGC 266
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 592)
Unang C. Kang, B., Gao, X., Xu, Z.,
                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 601)
Qian,B., Wu,T., Huang,Q., Huang,C., Kang,B., Gao,X., Xu,Z., Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Chen,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qian,B., Wu.T., Huang,Q., Huang,C., Kang,B., Gao,X., Xu,Z., Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang,Y., Gu,Y., Chen,Z. and Han,Z. Homo sapiens cDNA GLC clones
Unpublished (2000)
                                                                                                                      Contect: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                    AV719326.1 GI:10816478
EST.
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AV719326 GLC Homo sapiens
AV719326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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Chinese Mational Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
                                                                               Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                      Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                       Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
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Location/Qualifiers
1. .601
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/mol_type="mRNA"
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 604)

Olan, B., Mu, T., Huang, O., Huang, C., Kang, B., Gao, X., Xu, Z., Xiao, H., Xu, X., Li, N., Peng, Y., Liu, F., Qu, J., Song, H., Cheng, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Yang, Y., Gu, Y., Chen, Z. and Han, Z.

Homo appiens CDNA GLC clones
                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AV720014 GLC Homo sapiens
AV720014
                                                                                                                                                                                                                                                                                                                                                     Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai
                                                                                                                                                                                                                                                                                                                                                                                             Fax: 86-21-50801922
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Similarity 100.0%; F
76; Conservative 0;
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/lab host="SOLK"
/clome_lib="GLC"
                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue type="corresponding non cancerous liver tissue"
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                                                                                                                    /clone_lib="GLC"
/note="Vector: pBluescript sk(-); Site_1:
                                                                                                                                                                                                                              /clone="GLCCNG04"
                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                   8.8%; Score 76; DB 9; L
100.0%; Pred. No. 0.00033;
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;; Pred. No. 0.00033;
0; Mismatches 0;
  Mismatches
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206 AACTCCTGACCTCGTGATCCGCCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATG

265

68 AACTECTGACCTCGTGATCCGCCCGCCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATG 127

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RESULT 14
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    AUTHORS
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1 (bases 1 to 613)

Qian, B., Wu, T., Huang, Q., Huang, C., Kang, B., Gao, X., Xu, Z., Xiao, H., Xu, X., Li, N., Peng, Y., Liu, F., Qu, J., Song, H., Cheng, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Yang, Y., Gu, Y., Chen, Z. and Han, Z.

Homo sapiens cDNA GLC clones
Unpublished (2000)
Contact: Zerrania.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 AACTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATG 127
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613 bp mRNA linear EST 16-OCT-2000 AV720842 GLC Homo sapiens cDNA clone GLCCOHO5 5', mRNA sequence. AV720842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (1988) 1 to 481) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                       AGENCOURT 6567251 NIH MGC 88 Homo sapiens cDNA clone 5', mRNA sequence.
BM561574
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This clone is available at CHGC in Shanghai.
                                                                                                   Homo gapiens
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                                                                                                                           Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="corresponding non cancerous liver tissue"
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100.0%; Pred. No. 0.000;
ative 0; Mismatches
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                                                                                                                                          120 CAGGCATGAGCCAC 133
                                                                                                                                                                                       22 TGGTCTCGAACTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTA 81
                                                                                                                                                                                                                             60 TGGTCTCGAACTCCTGACCCCGTGATCCGGCCCGCCTCCCGAAAGTGCTGGGAATTA 119
                                                                                             82 CAGGCATGAGCCAC 95
                                                                                                                                                                                                                                                                                  74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov plate: LLAMI2753 row: j column: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution can be
                                                                                                                                                                                                                                                                                                              Similarity
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/clone_lib="NHH_MGC_88"
/note="Organ: small intestine; Vector: pCMV-SPORT6;
/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site_1: Not1; Site_2: Sall; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5739759"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . .481
                                                                                                                                                                                                                                                                                                         8.5%; Score 74; DB 12; 100.0%; Pred. No. 0.00088;
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Minimum DB seq length: 0
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1: geneseqn1980s:*
2: geneseqn1990s:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score 865.2	Query Match Length		2 1	ID AAX30367	Description Aax30367 DNA encod
, N	965.2	99.8) - 00	ω	ADB47729	Adb47729
n c	822.6	94.9	58181	-J -	ABZ56190	Abz74619
O (822.6	94.9	58181	o.	ADC21010	Adc21010
φ.	133.6	15.4	39703	9	ADC86430	Adc86430
c 7	133.6	15.4	134292	7	ACA64895	Aca64895
œ	130.4	0	22255	vı	AAH26497	Aah26497
9	130.4	15.0	115756	7	ACD13448	Acd13448
c 10	129.4	14.9	20951	σ	AAL53468	Aa153468
11	128.8	14.9	94191	φ	ADE11169_3	Continuation (4 of
c 12	128	14.8	407	σ	ABV12806	Abv12806
c 13	128	14.8	447	u	ABV03637	Abv03637
c 14	128	14.8	458	տ	ABV33935	Abv33935
c 15	128	14.8	458	ហ	ABV42808	Abv42808
c 16	127.8	14.7	307	4	AAK84065	Aak84065
c 17	127.8	14.7	5069	4	AAK67404	Aak67404
c 18	127.8	14.7	51959	თ	ABQ99650	Abq99650
	127.6	14.7	8960	4.	AAK69657	Aak69657
c 20	127.2	14.7	172	4.	AAK81214	Aak81214
	127	14.6	484	ſπ	ABV57673	Abv57673
c 22	126.8	14.6	121600	م	ABT10748	Abt10748
c 23	126.6	14.6	486	ດັນ	ABV49991	Abv49991

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125.4	125.4	125.4	125.4	125.4	125.4	125.6	125.6	125.6	125.8	125.8	126	126	126	126	126.2	126.2	126.2	126.2	126.2	126.2	126.6
14.5	14.5	14.5	14.5	14.5	14.5	14.5	14.5	14.5	14.5	14.5	14.5	14.5	14.5	14.5	14.6	14.6	14.6	14.6	14.6	14.6	14.6
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AAS40588	AAL06476	AAL36067	AAK79870	ABA16633	AAK79344	AAK89370	ABK69902	AAS28318	ABK83575	ABL86703	AAD26738	AAD26830	AAK84144	AAK84143	ADB70361	ABK84797	AAH18461	AAH10519	AAL05753	AAK84486	AAK86883
Aas40588 DNA encod		Human	Human	Human	Human	Human	Human				Human		Human	Human	Moesin	Abk84797 Human cDN	Human	Human	3 Human	Human	Human

ALIGNMENTS

RESULT 1 AAX30367 14-MAY-1999 (first entry) AAX30367; AAX30367 standard; DNA; 867 BP. DNA encoding a human secreted protein.

Secreted protein; cancer; tumour; neurodegenerative disorder; developmental abnormality; foetal deficiency; blood disorder; (NS disorder; immune system disease; autoimmune disease; hepatic disease; renal disease; inflammation; allergy; ischemic shock; Alzheimer's; cognitive disorder; schizophrenia; cardiovascular disorder; prostate disease; asthma; osteoporosis; arthritis; ss.

05-AUG-1997 05-AUG-1997 05-AUG-1997 05-AUG-1997 05-AUG-1997 05-AUG-1997 05-AUG-1997 05-AUG-1997 05-AUG-1997 05-AUG-1997 18-AUG-1997 18-AUG-1997 19-AUG-1997 19-AUG-1997 19-AUG-1997 19-AUG-1997 19-AUG-1997 19-AUG-1997 04-AUG-1998; 18-FEB-1999. WO9907891-A1. Homo sapiens. 19-AUG-1997 97US-0055386P. 97US-0055970P. 97US-0055986P. 97US-0056364P. 97US-0056366P. 97US-0056366P. 97US-0054798P. 97US-0054803P. 97US-0054804P. 97US-0055310P. 97US-0055311P. 97US-0055312P. 97US-0054809P 97US-0055309P 97US-0056371P. 97US-0056557P. 97US-0056370P 97US-0054806P 98WO-US016235

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conditions can also be diagnosed by determining the amount of the conditions can also be diagnosed by determining the amount of the conditions in the polymedides in a sample or by determining the presence of contrations in the polymucleotides. Specific uses are described for each of the products, based on which tissues they are most highly expressed in, conditions in the polymucleotides. Specific uses are described for each of the products, based on which tissues they are most highly expressed in, conditions and include developing products for the diagnosis or treatment of cancer, conditions and contract of the con
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Matches 867
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19-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 867 BP; 219 A; 231 C; 222 G; 192 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The specification describes secreted proteins and their corresponding polynucleotides which are useful for preventing, treating or ameliorating
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            GCTTTGAAAGGGGCAGAAGTATAGTGGGCGAGCTGCCCACCTGCTACAGTGAAGGGATCT
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97US-0056731P.
97US-0056732P.
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481 AATGACCCCACGGGAGCTTACACAAGTYCAAACAGGCCCAAATGCATTCATGAGCAGGGG 540
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                        TGCTATGACCAATCTCGTGCCGAATTC 867
                                                                               GCCACTCGGATTTGAACCCCGGCTCCTCAAGGTCAGCTGTGTAGCCTTGANTGAAYCACC
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ADB47729 standard; cDNA; 867 BP

(first entry)

Novel human secreted protein cDNA #2.

superoxidase; SOD; catalase; DNA repair protein; oncogene; tumour suppressor; tumour necrosis factor; TNF; inflammation; blood vessel growth inhibition; immune response; immune system disorder; hyperproliferative disorder; neoplasm; cardiovascular disorder; hyperproliferative disorder; neoplasm; cardiovascular disorder; peripheral artery disease; limb ischaemia; arterio-arterial fistula; peripheral artery disease; limb ischaemia; arterio-arterial fistula; reovascularisation disorder; wound healing; neurological disease; Alzheimer's disease epithelial cell proliferation; neurological disease; Alzheimer's disease infectious disease. Parkinson's disease; Huntington's disease; mania; dementia; human; secreted protein; insulin; haemoglobin S; haemoglobin B;

04-OCT-2001; 2001US-00969730.

97US-0054808P.
97US-0054809P.
97US-0055309P.
97US-0055310P.
97US-0055311P.
97US-0055312P.
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97US-0055312P. 97US-0054804P.

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cc absent or decreased levels of polypeptides e.g. insulin, to supplement or decreased levels of different polypeptides, e.g. haemoglobin S con for haemoglobin B, superoxidase (SDD), catalase, DNA repair protein, to con inhibit the activity of a polypeptide e.g. an oncogene or tumour controlled the activity of a polypeptide e.g. an oncogene or tumour controlled the activity of membrane bound receptor by competing controlled the activity of membrane bound receptor by competing controlled in reducing inflammation, or to bring about a desired cresponse e.g. blood vessel growth inhibition, enhancement of immune controlled the response to proliferative cells or tissues. The protein and the nucleic continuous system involving abnormal growth of specific types of cells as of other cell types where expression has been observed. The protein, the nucleic acid and antibodies are useful for treating, preventing, detecting, diagnosing disorders (contains system, hyperproliferative disorders including meoplasms, contained arterio-arterial fistula as peripheral artery disease, limb cardinal cell proliferation, neurological diseases (such as Alzheimer's disease, parkinson's disease, Huntington's diseases (such as Alzheimer's etc), infectious diseases caused by virus, bacteria, fungi, etc. The contains accorded to the contains and contains and contains and contains and contains accorded to the contains and contains a contains and contains an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosing pathological condition or a susceptibility to pathological condition in a subject. The protein is useful as reagents for differential identification of the tissues or cell types present in a biological sample. The protein can be administered to patients having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel human secreted proteins. The protein i useful for preventing, treating or ameliorating a medical condition protein is useful for diagnosing a pathological condition or susceptibility to a pathological condition in a subject. The protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human secreted proteins useful for treating and/or diagnosing disorders of immune system, cardiovascular disorders such as peripheral artery disease, neurological diseases such as Alzheimer's disease.
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19-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 205; 333pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              artery disease, neurological diseases such as Alzheimer's
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19-AUG-1997;
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GREENE J M.
FERRIE A M.
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ROSEN C A.
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JANAT F.
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98WO-US016235.
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J, Rosen CA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              481 AATGACCCCACGGGAGCTTACACAAGTYCAAACAGGCCCAAATGCATTCATGAGCAGGGG
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TGCTATGACCAATCTCGTGCCGAATTC
                                                                                        GCCACTCGGATTTGAACCCCGGGCTCCTCAAGGTCAGCTGTGTAGCCTTGANTGAAYCACC
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; Pred. No. 2.1e-247;
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RESULT 3 ABZ68140/c ID ABZ681 XX

ABZ68140 standard; DNA; 58181

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Best Local S
Matches 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    virucide; dermatological; immunosuppressive; antiinflammatory; anti-HIV; vulnerary; antibacterial; antiparkinsonian; antisticking; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; infection; vaccine; cardiovascular disorder; neurological disease; nephrotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human secreted proteins encoded by genes contained in cDNA clones (e.g. HGCAC19), useful for preventing, treating or diagnosing e.g. AIDS, multiple sclerosis, herpes virus, leukemia, tick-borne encephalitis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-MAR-2001; 2001US-0278650P.
12-SEP-2001; 2001US-00950082.
12-SEP-2001; 2001US-00950083.
                                                                                                                                                                                                                                                                                                                  Sequence 58181 BP; 15503 A; 12755 C; 13504 G; 16419 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      West Nile fever.
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                                                                                                                                                                                                                                                        Similarity
                                                                                                      CGAACTCCTGACCTCGTGATCCGCCCGCCTCGGGCTCCCAAAGTGCTGGGATTACAGGCA 125
    TGAGCCACTGCGCCCAGCCGGTCTTTTTAAACATTCCCCAGGACTGTACAGCCAACCCAT 52386
                       TGAGCCACTGCGCCCAGCCGGTCTTTTTAAACATTCCCCAGGACTGTACAGCCAACCCAT 185
                                                                                                                                                             TITTITTTTTTTTTTTTTAAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATGGTCT
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99.38;
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                                                                                                                  AGAGCAGAGGTGGGCAGGCCCTTTTGATTAATGTATCATTCTTGAATGCAAGCTTCAAAA
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                                                            TATGACCAAT 51716
                                                                                        TATGACCAAT 853
                                                                                                                                               GGGCCGACTGGCCAGAGACAGATCCGCAAGAGCCTCTGCAGCTCTGGTGCCAAGCC
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ABZ74619 standard; DNA; 58181

12-MAY-2003 (first entry)

Secreted protein gene 372 genomic fragment HWBCN36, SEQ ID NO:1766.

Human; secreted protein; cancer; tumour; hyperproliferative disorder; autoimmune disorder; inflammation; angiogenic diseases; AIDS; acquired immunodeficiency syndrome; hepatitis; anaemia; wound healing; drug screening; chromosome identification; chromosome mapping; cytostatic; gene therapy; antiinflammatory; immunomodulator; vulnerary; gene; ds. anti-HIV;

Homo sapiens.

WO200277013-A2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 58181 BP; 15503 A; 12755 C; 13504 G; 16419 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identification, chromosome mapping, in gene therapy, for identifying individuals from minute biological samples, as hybridisation probes, and as molecular weight markers. The present sequence represents a human secreted protein genomic fragment referred to in the disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein genes, and ABP00947-ABP01363 represent the proteins they encode. ABZ73598-ABZ74687 represent human secreted protein genomic fragments. The invention also encompasses antibodies specific for the secreted proteins, the use of the secreted proteins in drug screening and recombinant vectors and host cells comprising a nucleic acid of the invention. The secreted proteins are thought to be involved in biological activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human secreted proteins and nucleic acids, useful for detecting or treating cancer or other hyperproliferative disorders, autoimmune disorders, inflammatory disorders, HIV disease, hepatitis or anemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 2331-2345; 2474pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-040578/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABZ73281-ABZ73697 represent cDNAs corresponding to 391 human secreted
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                                                                                                                                                                                                                                                                                                                            52445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52565 TITTITTTTTTTTTTTTTTTTAAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATGGTCT
                                                                                                                                                                                                                                            52385
                                                                                                                                                                                                                                                                                     186
                                                                                                                                                                                                                                                                                                                                                                       126
366 GAAAGGGGCAGAAGTATAGTGGGCGA-GCTGCCCACCTGCTACAGTGAAGGGATCTGGAG
                                                                                                                                                                                           844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 ITTTTTTTTTTTTTTTTTTTAAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATGGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                       TCAGCGAACAAAAGCCTCTAGGTCTTTCTTACCACAAACACCTCTCTGCCCACCTGCTTT
                                                                                                TCAGCGAACAAAGCCTCTAGGTCTTTCTTACCACAAACACCTCTCTGCCCACCTGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGAACTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCA 125
                                                                                                                                                                                                                                            ACTCACCTGACATTTGGGAACTCCCCCCCACGGCCATAACTGATCTGCAGAGGTAAGACC
                                                                                                                                                                                                                                                                                                                            TGAGCCACTGCGCCCAGCCGGTCTTTTTAAACATTCCCCAGGACTGTACAGCCAACCCAT 52386
                                                                                                                                                                                                                                                                                                                                                                       TGAGCCACTGCGCCCAGCCGGTCTTTTTAAACATTCCCCAGGACTGTACAGCCAACCCAT 185
                                                                                                                                                         ACTCACCTGACATTTGGGAACTCCCCCCCCACGGCCATAACTGATCTGCAGAGGTAAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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2001US-00950082
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99.3%;
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Pred. No. 6.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                gene therapy; human; secreted protein; haemopoietic disorder; haematological disorder; anaemia; haemophilia; inflammatory disorder; inflammatory bowel disease; Crohn's disease; neoplastic disease; cancer; leukaemia; wound healing; epithelial cell proliferation disorder; leukaemia; wound healing; epithelial cell proliferation disorder; immune disorder; autoimmune disorder; autoimmune disorder; autoimmune disorder; atherosclerosis; myocardiis; cardiovascular disorder; atherosclerosis; myocardiis; infectious disease; HIV; AIDS; endocrine disorder; diabetes;
                                                                                                                       27-MAR-2001; 2001US-0278650P
12-SEP-2001; 2001US-00950082
12-SEP-2001; 2001US-00950083
                                                                                                                                                                                                                                                                                                                   gastrointestinal disorder; duodenal ulcer; gastroenteritis; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted protein-related DNA sequence #428.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-2003
                             WPI; 2003-129287/12.
                                                                                                                                                                                        26-MAR-2002; 2002WO-US009257
                                                                                                                                                                                                                        21-NOV-2002
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                                                                                             (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 485 ACCCCACGGGAG-CTTACACAAGTYCAAACAGGCCCAAATGCATTCATGAGCAGGGGGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATGACCAAT 51716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTOGGATTTGAACCCCGGCTCCTCAAGGTCAGCTGTGTAGCCTTGANTGAAYCACCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCAAAGGACTCCGGAGGAGAGAGGGCCCAATAAGGCTGGTGCTATTTCCGATCCATAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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New human secreted proteins and nucleic acid molecules, useful

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Best Local !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for detecting, preventing, diagnosing, prognosticating, treating or ameliorating: haematopoietic or haematological disorders (e.g. anaemia and haemophilia); inflammatory disorders (e.g. inflammatory bowel disease and Crohn's disease); neoplastic disease (e.g. cancer and leukaemia); wound healing and disorders of epithelial cell proliferation; immune disorders (e.g. autoimmune disorders and asthmatic disorders); cardiovascular disorders (e.g. atherosclerosis and myocarditis); infectious disease (e.g. HIV/AIDS); endocrine disorders (e.g. diabetes); and gastrointestinal disorders (e.g. dividenal ulcers and gastroenteritis). The present DNA sequence was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention comprises the amino acid and coding sequences of human secreted proteins. The DNA and protein sequences of the invention are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 964; 1512pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preparing a diagnostic or pharmaceutical composition for diagnosing, preventing or treating hematopoietic or hematologic disorders, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 58181 BP; 15503 A; 12755 C; 13504 G; 16419 T; 0 U; 0 Other;
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                                                                                                                                                  AGAGCAGAGGTGGGCCGCTTTTGATTAATGTATCATTCTTGAATGCAAGCTTCAAAA 663
                                                                                                                                                                                                                                                                          GCCAAAGGACTCCGGAGGAGAGGGCCCAATAAGGCTGGTGCTATTTCCGATCCATAGAG 603
                                                                                                                                                                                                                                                                                                                              <u> ACCCCACGGGAGCCTTACACAAGTCCAAACAGGCCCAAATGCATTCATGAGCAGGGGGAG</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAAGGGGCAGAAGTATAGTGGGCGA-GCTGCCCACCTGCTACAGTGAAGGGATCTGGAG
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TCCGGGTATGCCGGGTGAGAATGAGCAGGACTAACACCTGGGTGTCATGGCAAGCCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCAGCGAACAAAAGCCTCTAGGTCTTTCTTACCACAAACACCTCTCTGCCCACCTGCTTT
                                                                                                                                                                                                                                                                                                                                                                             ACCCCACGGAG-CTTACACAAGTYCAAACAGGCCCAAATGCATTCATGAGCAGGGGGAG
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                                                                                                                                                                         The invention relates to a novel polynucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The polynucleotide sequences shown in ADCB5548-ADCB7616 encode GPCR's of the
                                                                                                                                     Sequence 39703 BP; 10210 A; 8488 C; 9860 G; 11145 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP1270724-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                guanosine triphosphate-binding protein coupled receptor; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human GPCR gene SEQ ID NO:883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADC86430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADC86430 standard; DNA; 39703
                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 883; 28pp; English.
                                                                                                                                                                                                                                                                                                              guanosine triphosphate-binding protein coupled receptor.
                                                                                                                                                                                                                                                                                                                               New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUN-2001; 2001JP-00246789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JUN-2002; 2002EP-00013517.
                                                                                                                                                                                                                                                                                                                                                                      P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene; human; GPCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         784 ACTCGGATTTGAACCCCGGCTCCTCAAGGTCAGCTGTGTAGCCTTGANTGAAYCACCTGC 843
                                                                                                                                                                                                                                                                                                                                                                                     2003-315783/31
                                                                                  139;
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                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                         CENT ADVANCED SCI & TECHNOLOGY
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                              TTTTTTTTTTTTTTTTTTTTAGTAGAGACGGGGTTTCACCGTGTTAGCCAGGATGGTCT 11046
                                              TTTTTTTTTTTTTTAAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATGGTCT
 CGAACTCCTGACCTCGTGATCCGCCCGGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCA 125
                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                               Akiyama Y,
                                                                                               15.48;
                                                                                  Ö
                                                                                               Score 133.6; DB 9
Pred. No. 1.5e-28;
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                                                                                                                                                                                                                                                                                                                                                                                                               Aburatani H;
                                                                                   Mismatches
                                                                                                            DB 9;
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                                                                                                            Length 39703;
                                                                                     Indels
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RESULT 7
ACA64895/c
                                                                                                                                                                                                      Matches 139;
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Best Local
                                                                                                                                                                                                                                                                                                                                   This invention describes a novel reagent for diagnosis, molecular definition and therapy of chronic inflammatory joint diseases, and other inflammatory disorders, infective or tumour diseases in humans. The products of the invention have antiinflammatory, cytostatic, antirheumatic and immunosuppressive activity and can be asset for gene therapy. The reagent of the invention and any proteins and antibodies derived from it, are used (i) for analysing tissue and blood samples for medical diagnosis; (ii) for diagnosis and characterisation of chronic joint diseases, on the basis of molecular characterisation, and determining the etiological pathogenicity principle of as yet uncharacterised inflammatory diseases, also monitoring progression and/or treatment of disease, and optimisation of therapy and (iii) for developing treatments for inflammatory diseases, particularly of joints, infections and tumours. ACA64801-ACA64965 represent human polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; chronic inflammatory joint disease; infection; tumour; antiinflammatory; cytostatic; antiarthritic; antirheumatic; immunosuppressive; gene therapy; etiological pathogenicity; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACA64895 standard; DNA; 134292 BP
                                                                                                                                                                                                                                                                             Sequence 134292 BP; 38020 A; 31344 C; 29670 G; 35258 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reagents for diagnosis, study and therapy of chronic inflammatory joint and other diseases, comprises any of many specified genes or derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human GABBRI DNA corresponding to AL031983.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page; 12pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-240797/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haeupl T, Ungethuem U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PATH-) PATHOARRAY GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2001; 2001DE-01027572
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                                                                                                                                                                                                                                                                                                                          used in the method of the invention
                                    113339 CGATCTCCTGACCTCGTGATCCGCCCGCCCTCGGCCTCCCCAAAATGCTGGGATTACAGGCG 113280
                                                                                                                    113399 TTTTTTTTTTTTTTTTTTTTAGTAGAGGGGGTTTCACCGTGTTAGCCAGGATGGTCT 113340
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126 TGAGCCACTGCGCCCAGCCGGTCTTTTT 153
                                                              66 CGAACTCCTGACCTCGTGATCCGCCCGCCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCA 125
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                                                                                                                                                                                                                         Similarity
                                                                                                                                              TTTTTTTTTTTTTTAAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATGGTCT 65
                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                     15,48;
93,98;
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                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                       Score 133.6; DB 7;
Pred. No. 2.5e-28;
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AAH26497
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                                               02-MAR-2000; 2000US-00517849.
14-JUL-2000; 2000US-00616289.
                                                                                                       28-FEB-2001; 2001WO-US006356
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          (BOST-) BOSTON HEART FOUND INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH26497;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Low density lipoprotein binding protein 3; LBP-3; LDL; human; atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
                    intron
                                                           intron
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens
                   15898
                                                                                                                                                                                                                                                                                                                                                      2269
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RESULT 9
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Best Local S
Matches 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                            Human; ds; gene; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic; antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer; lung cancer; ovarian cancer; angiogenesis; cell cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22255 BP; 5195 A; 5302 C; 5924 G; 5834 T; 0 U; 0 Other;
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                                                                          05-JUN-2001; 2001US-0296076P.
10-OCT-2001; 2001US-0328605P.
                                                                                                                                                                                                       12-DEC-2002.
                                                                                                                                                                                                                                                                                                                                                    apoptotic disorder; cell proliferation disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human DNA encoding a p53 modifier, SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACD13448;
                                                                                                                                                    03-JUN-2002; 2002WO-US017382
                                                                                                                                                                                                                                                       WO200299122-A1
                                                     15-FEB-2002;
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                                                       2002US-0357253P
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89.7%;
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Pred. No. 1.1e-27;
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Friedman L,
                                                     Plowman
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                                                     Belvin M,
                                                     Francis-Lang H,
                                                     Li D,
                                                     Funke RP;
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AB007223.

pathway in Drosophila. Identifying modulators of the p53 pathway for use in treating apoptotic or cell proliferation disorders, comprises screening for agents that modulate activity of a human ortholog of genes that modify the p53

Example 2; Page 320-351; 678pp; English.

Commodulating agent, by contacting an assay system comprising a purified HM compacting on mucleic acid with a test agent under conditions, where but the presence of the test agent, the system provides a reference condition, where but contacting a cell defective in p53 pathway in contacting a cell defective in p53 pathway of a cell (comprising contacting a cell defective in p53 pathway contacting a cell defective in p53 function with a candidate modulator contacting a cell defective in p53 function with a candidate modulator contacting an endulator that specifically binds to a HM polypeptide comprising an HM amino acid comprising contacting the cell (comprising contacting the cell with an agent that specifically binds an HM polypeptide comparising an HM amino acid compression; (c) comparising contacting the cell with an agent that compression; (c) comparising the results with a control; and diagnosing (M4) contacting the sample with a probe for HM comparison indicates a likelihood disease). (M1) is useful contentifying modulators of the p53 pathway. A probe for HM expression contentifying modulators of the p53 pathway. A probe for HM expression contentifying modulators of the p53 pathway. A probe for HM expression contentifying modulators of the p53 pathway. A probe for HM expression contentifying modulators where disease or disorder prognosis is related to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell contentified by (M1) are useful in a variety of diagnostic and contentified by (M1) are useful in a variety of diagnostic and contentified by (M1) are useful in a variety of diagnostic and contentified by (M1) are useful in a variety of diagnostic and contentified by (M1) are useful in a variety of diagnostic and contentified by (M1) are useful in a variety of diagnostic and contentified by (M1) are useful in a variety of diagnostic and contentified by (M1) are useful in a variety of diagnostic and contentified by (M1) are useful in a variety of diagnostic and contentified by (M1) are useful The invention relates to identifying (MI) a candidate p53 pathway nucleic acid encoding a p53 pathway modifying protein

Sequence 115756 BP; 29575 A; 26665 C; 27977 G; 31539 T; 0 U; 0 Other;

Length 115756;

δ 당 S á 멼 닭 Matches 140; Query Match Best Local : Local Similarity 75009 74949 126 66 თ rcaccaccaccicracicratriatriatriatric 75044 TGAGCCACTGCGCCCAGCCGGTCTTTTTAAACATTC 161 CGATCTCTTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCT 75008 CGAACTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCA TTTTTTTTTTTTTTTTTTTAGTAGAGACGGGGTTTCACCGTGTTAGCCAGGATGGTCT TTTTTTTTTTTTTTTTTAAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATGGTCT Conservative 15.0%; 89.7%; 0 Score 130.4; DB 7; Pred. No. 2.1e-27; Mismatches 16; Indels 0 Caps 74948 65 0

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                                              AAL53468/c
                                                    RESULT 10
                                         AAL53468 standard; DNA; 20951
                               AAL53468
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Genomic DNA encoding human Ras-like protein.

16-JAN-2003

(first entry)

Human; Anti-HIV; neuroprotective; nootropic; cerebroprotective; cardiant;

1111	177	7 T	1111	1777	1 1 1 1 1 1	11 H H	1777	333	777	H H H	11 11 1	1111	17 7	11.1	777	F 1 1	H H H	H H H	11 11 11 11 11 11 11 11	17 2 3	8 8 X	꽃꽃꽃	결결결	222
variation	intron	S	intron	exon	variation	variation	intron	exon	variation	Variation	Incron	exon.		in the second	exon	intron	exon	intron	exon	Key	ens.	<pre>viral infection; stroke; toxin-in hepatitis C; ost;</pre>	genetic immunodeficio Parkinson's disease; cerebellar degenerati	ophthalmological; immunomodulator; dene therapy; hum
/ number= / replace(6799,T) /*tag= ai		/+tag= n /number= 7	/+tag= m /number= 6	60576230 /*tag= 1 /number= 6	replace(602,G) /*tag= ah2,G) /standard_name= "Single_nucleotide_polymorphism"	replace(spo., 1) /*tag= ag /standard_name= "Single nucleotide polymorphism"	1854 6056 1864	/*tag= 5 /rumber= 5	replace to one / or / *tage as of /*tage as of /*tage as of / standard_name= "Single nucleotide polymorphism" / standard_name= "Single nucleotide polymorphism"	<pre>replace(300,6) /*tage as /standard_name: "Single nucleotide polymorphism"</pre>	/#teg= 4 /#umber= 4	/*teg= .** /*teg= /* /number= /*	/*tag= g /number= 3	/*tag= f /number= 3 4428	/*tag= e /number= 2 43644427	/*tag= d /number= 2 38564363	/*tag= c /number= 1 37543855	/*tag= b /number= 1 30733753	''.'ay a'' /product= "Human Ras-like protein" /note= "Coding sequence contains 14 introns" 30003072	급임		fection; myocardial infarction; alcohol-induced liver damage; toxin-induced disease; lathyrism; cachexia; hepatitis B; cancer; s C; osteoporosis; transgenic animal; hepatotropic; gene; ds.	aunodeficiency; neurodegenerative disease; Alzheimer's disease; disease; amyotrophic lateral sclerosis; retinitis pigmentosa; degeneration; aplastic anaemia; ischemic injury; cirrhosis;	ophthalmological; antiinflammatory; antianaemic; vasotropic; immunomodulator; virucide; cytostatic; osteopathic; Ras inhibitor; AIDS; gene therapy; human Ras-like protein; cell proliferation; apoptosis;
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/*tag= as /standard_name=	<pre>/*tag= ac /number= 14 replace(18059,G)</pre>	. 27	. 2	/standard_name= /standard_name= replace(16756,G) /*tag= ar	மை	4 7	. 7	. 7	. 7	, μ	6 53	<pre>/standard_name= replace(14723,C) /*tag= an</pre>	<pre>/number= 11 replace(12025,G) /*tag= am</pre>	1075515675 /*tag= ¥		/number= 10 1032510638 /*tag= u /number= 10	ᅺᇊ	<pre>/number= y replace(10159,C) /*tag= al /standard name=</pre>		/standard_name= 98869963 /*tag= r		ட் வ ம	/110mber= 6 91159885 /*tag= q /mumber= 8	

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      Continuation (4 of 4) of ADE11169 from base 300001
WP Sequence split into 4 fragments LOCUS ADE11169
WP Fragment Name Begin End
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                                                                                                                  ADE11169
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel human Ras-like protein comprising a fully defined sequence of 615 amino acids, given in the specification, its allelic variant, orthologue or its fragment comprising at least 10 contiguous amino acids. The new human Ras-like proteins and the polypeptides encoding them are useful in the diagnosis, prevention, and treatment of inflammation and disorders associated with cell and the polypeptides encoding them are useful in the diagnosis, prevention, and treatment of inflammation and disorders associated with cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neurodegenerative diseases, ischemic injurviral infections, cancer and osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated Ras-like protein polypeptides, useful for treating AIDS, neurodegenerative diseases, ischemic injuries, toxin-induced diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Fig 3A-G; 91pp; English
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Fragment Name
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ADE11169 1
ADE11169 2
ADE11169 3
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                                                                                                                                                                                                                                                                                 GAACTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCAT 126
                                                                                                                                                                                    GAGCCACCGCCCCGGCCTGTCCCTTCTTATTATCCCACCAC 17114
                                                                                                                                                                                                                                                                                                                                         TTTTTTTTTTTTTTTAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATGGTCTC
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/*tag= at
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87.1%;
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310000
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                                                                                    se 300001 (Human transporter protein ADE11169 Accession Ade11169
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ABV12806/c
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Best Local :
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16-MAR-2000; 2000US-0189862P.
25-MAY-2000; 2000US-0207454P.
09-JUN-2000; 2000US-0211314P.
18-JUL-2000; 2000US-0219007P.
13-DEC-2000; 2000US-0255281P.
                                               The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is affilicted with prostate cancer; (b) monitoring the efficacy progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (f) assessing the prostate cancer has metastasized in a patient; (h) determining whether prostate cancer has metastasized cancer in a patient; (f) assessing the aggressiveness or indolence of prostate cancer in a patient.
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                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
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                                                                                                                                                                                                                                                                                       Claim 1; Page 2109; 11750pp; English
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                                      (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
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Pred. No. 5.8e-27;
0; Mismatches 22;
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Query Match

Sequence 407 BP; 124 A; 111 C; 81 G; 91 T; 0 U; 0 Other;

Score 128;

띮 <u>ເ</u>ກ

Length 407

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RESULT 13
ABV03637/c
ID ABV036
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Query Match
Best Local Similarity
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16-MAR-2000;
25-MAY-2000;
                                                                                             The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables I-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (f) assessing the prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastabled in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient assessing the aggressiveness or indolence of prostate cancer in a patient.
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                                               Sequence 447 BP; 126 A; 121 C; 100 G; 97 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                        Claim 1; Page 653; 11750pp; English.
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                                                                                (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
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2000US-0207454P.
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2000US-0219007P.
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14.8%;
93.1%;
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 Score 128; DB 5
Pred. No. 1e-27;
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                             a nuclectide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is affilicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cell carcinogenic potential of a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient in a patient of the prostate cancer has metastasized in a patient of a compound; (g) assessing the aggressiveness or indolence of prostate cancer in a patient of a compound; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
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25-MAY-2000;
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2000US-0189862P.
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Query Match Best Local Similarity

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16-MAR-2000; 2000US-0188862P.
25-MAY-2000; 2000US-0207454P.
09-JUN-2000; 2000US-0211314P.
18-JUL-2000; 2000US-0219007P.
13-DEC-2000; 2000US-0255281P.
                                                                 The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cell carcer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
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Query Match Best Local 9

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ALIGNMENTS

TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KBYWORDS	VERSION	ACCESSION		DEFINITION	Locus	HS888M10/c	RESULT 1
Direct Submission	Cobley, V.	1 (bases 1 to 124874)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	Homo sapiens (human)	HTG.	AL031296.1 GI:4106564	AL031296	1p36.11-36.31, complete sequence.	Human DNA sequence from clone RP5-888M10 on chromosome	HS888M10 124874 bp DNA linear PRI 04-MAR-2003		

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Best Local Similarity
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPOG; Tr:, TREMBL; Wp:, WORMPBP; Information on the WORMPBP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1 constructed by the Sanger Centre Chromosome 1 Manning
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                                                                                                                                                                                                                                                                                                                                                                          87225 CGAACTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jan 5, 1999 this sequence version replaced gi:3881974.
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TGAGCCACTGCGCCCAGCCGGTCTTTTTAAACATTCCCCAGGACTGTACAGCCAACCCAT 185
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/mol_type="genomic DNA"
/db_xref="RZPD:RPCIP704M10888"
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Pred. No. 9.7e-240;
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Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-395, Pax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library
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Kodaira, H., Furiya, T., Takahashi, M., Kikkawa, E., Omura, Y., Abe, K.,
Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M.,
Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishi, S.,
Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T.,
Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M.,
Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi-Pujii, A.,
Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
Nagahari, K., Masaho, Y., Nagai, K. and Isogai, T.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                           Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On May 14, 1999 this sequence version replaced gi:4808231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (04-MAR-2003) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complete sequence. AL031427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human DNA sequence from clone RP1-167A19 on chromosome 1p32.1-33.
                                                                                                                                                                                                                           Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                      Center code: SC
                                                                                                                                                                                                                                                                                                                Center: Wellcome Trust Sanger Institute
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                                                                                                                                                                                                                                                        site: http://www.sanger.ac.uk
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/clone_lib="D3CST2"
/note="cloning vector: pME18SFL3~mRNA from CD34+ cells
after 3-days ODF induction.-primary culture, CD34+ Cells"
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/db_xref="taxon:9606"
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw., SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/ChrI
RPI-167A19 is from the library RPCI-1 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127493 A 127493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VECTOR: PCYPAC2
                                                    Guandsine triphosphate-binding protein coupled receptors Patent: EP 1270724-A 883 02-GAN-2003, National Institute of Advanced Industrial Science and Technology (JP); Center for Advanced Science and Technology Incubation, Ltd.
                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 883 from Patent EP1270724.
                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
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/mol_type="genomic DNA"
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Pred. No. 1.7e-30;
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Submitted (11-JUL-2001) Makiko Suwa, Computational Biology Research Center (CBRC), National Institute of Advanced Industrial Science and Technology (ALST); 2-41-6 Aomi Koto-ku, Tokyo 135-0064, Japan (E-mail:m-suwa@aist.go.jp, URL:http://www.cbrc.jp/,
                                                                                                                                                                                                                          Suwa,M., Sato,T., Okouchi,I., Arita,M., Futami,K., Matsumoto,S., Tsutsumi,S., Aburatani,H., Asai,K. and Akiyama,Y. Genome-wide discovery and analysis of human seven transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens gene for seven transmembrane helix receptor, complete cds, isolate:CBRC7TM_39.
                                                                                                     Suwa, M.
Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PLAYDAIWALALALNKTSGGGRSGVELEDENYNNOTITDQITRAMNSSSFEGVSGHV
VFDASGSRMAWTLIFQLQGGSYKXIGYXDSTKDDLSWSKYTDKNIGSPPADQTLAL
FRFLQKLFIEVSVELSSIGIVLAVVCLSFNIVNSHVRYIQNSQPNLANLTAVGCSLAL
AAVFPLGLDGYHIGRNQFPFVCQARLWLLGLGFSLGYGSMFTKIWVHTVFTKKEEKK
EWRKTILEPWKLYATVGLLVGMDYLTLAIWQIUDPLHRTIEVPLERRCYGQENEGGSVA
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hpsserravyigalfprsggmpggacqparledvnsrrdiiddsk
valdmgcdpfgartkylybllyndfkiiimpgcssvsfilvabaarmmiilvlysgss
palsnrgrpfffffhsatilandfrvklerkmgkkklatiQqttevftstlddleer
vkeagieiffrqsffsdparvknikkyykerlekkyvmfligvtsvmfkiidpsin
vkeagieiffrqsffsdparvknikkyykerlekkyvmfligvingkiidpsin
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14506. 14748,15377. 15440,16990. 17067,18612. 18762,
19258. 19390,20773. 20889,20987. 22167,22295. 22422,
23003. 23131,23354. 23497,24275. 224444,39365. 39503)
/note="unnamed protein product"
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TMI LSSQQDAAFAFASLAI VFSSY I TLVVLFVPKMRRL I TRGEHQSEAQDTMKTGSST
NNNEBEKSRLLEKENRELEK I I AEKEERVSELAHOLOSROOLRSRRHPFYFPEPEGGGL
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/db_xref="GI:28799075"
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/db_xref="taxon:9606"
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          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Similarity 93.9%;
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11107 TGAGCCACCGCGCCCAGCCTTTTTTTT 11134
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Location/Qualifiers
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This sequence is a seven transmembrane helix receptor candidate predicted from the whole human genome sequences using our automated system that contains programs of gene finding (GeneDecoder), sequence search, motif-domain assignment and transmembrane helix prediction.

And the sequence is submitted by the collaborative project between the project between the contains and the sequence is submitted by the collaborative project between the contains and the sequence is submitted by the collaborative project between the contains and the sequence is submitted by the collaborative project between the contains and the sequence is submitted by the collaborative project between the contains and the sequence is submitted by the collaborative project between the contains and the contains are contained to the contains and the contains are contained to the contains and the contains are contained to the conta
                                                                                                                           AP000079 100000 bp DNA linear PRI 07-J Homo sapiens genomic DNA, chromosome 8p11.2, senescence gene region, section 15/19, complete sequence.
AP000079.1 GI:4580000
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VALDMGCDPGQATKYLIFELLYNDPIKTILMPGCSSVSTLVARBAARMANLIVLSYGSSS
PALSINGCDPGQATKYLIFELLYNDPIKTILMPGCSSVSTLVARBAARMANLIVLSYGSSS
PALSINGCDPGQATKYLIFELLYNDPIKTILMPGCSSVSTLVARBAARMANLIVLSYGSSS
PALSINGCPPTFFRTHPSATILHDPIKYLFEKMGMKKIATIQQTTEVTSTLDDLBER
VKEAGLISITTRQSFFSDPAVPVKNLKYYKERLJEGKKYWFLIGWYADNWFKIYDPSIN
CTVDEMTEAVBGHITTEIVHLMPANTRSISHMTSQEFVEKLTKRLKHFEETGGPQEA
PLAYDAIWALALALNKTSGGGRSGVRLEDFNYMOTITDQIYEAMNSSSFBGVSGHV
VFDASGSRMAMTLIEQLQGGSYKXIGYYDSTKDDLSYGSTDKHIGGSPPADQTLVIKT
FRFLSQKLIFISVSUSIGITLAVVCLSFNIYNSHTNZYJONSQPHLNNLTAVGCSLAL
AAVPPLGLDGYHIGRNQFPFVCQARLMILGGIGFSLGYGSMFTKIWWVHTVFTKXZBKX
EWRKTLSPMKLYATVGLLVGKDVLTLAIWQIVDPLHRTIEVPLERCYGCDENEQGSVA
IRALGLCIFYGYKGLLLLGIFLAYETXSVSTRKINDHAAVGWAIYNAVLCLITAPV
TMILESGQDAAPAFASLAIVFSSYITLVVLIVPWARRLITRGEWGSBADDTKNTGSST
NNNEEESKRLLEKSENRELEKIIAEKERVSLHHQLSGSQCLRSRRHPPTPPBPBSGGL
PRGPPBPBRLSCDGSRVHLLYKVNPQHCPGNGSVRDXDEAERHNQDBDTGNSHLDLI
FRGPPBPBRLSCDGGSRVHLLYKVNPQHCPGNGSVRDXDEAERHNQDBDTGNSHLDLI
FRGPPBPBRSCDGSRVHLYKVNPQHCPGNGSVRDXDEAERHNQDBDTGNSHLDLI
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/protein_id="BAC05730.1"
/db_xref="GI:21928257"
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/isolate="CBRC7TM_39"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 CCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Japan Science and Technology Corporation (JST) 5-3, Yonbancyo, Chiyoda-ku, Tokyo, 102-0081 Japan For further infomation about this sequences, please visit our sequence archive Web site (http://www-alis.tokyo.jst.go.jp/HGS/top.html) or send email to webmaster@www-alis.tokyo.jst.go.jp.
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This sequence is conducted by Japanese Foundation for Cancer
Submitted (24-JUN-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. B-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk Cn Jun 24, 2003 this sequence version replaced gi:32168690.
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Principal Investigator: Yusuke Nakamura Ph.D
Phone:+81-3-5449-5372, Fax:+81-3-5449-5433,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         yusuke@hgc.ims.u-tokyo.ac.jp
The sequence is submitted by Human Genome Sequencing in ALIS
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2 (bases 1 to 100000)
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DNA sequence analysis of a 1.9-Mb region on chromosome 8p11.2
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                                                                                                          Direct Submission
                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                 Homo sapiens (human)
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                                                                                                                                                         (bases 1 to 102684)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /map="8p11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .10000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.4%;
76.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 133.6; DB 9;
Pred. No. 3.2e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                           102684 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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RESULT 8
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                                                                                                                                                                                                    KEYWORDS
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                                                                                                                                              ORGANISM
                         AUTHORS
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Bm. EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp.; WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs constructed by the MHC Haplotype Consortium and collaborators. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84698 TTTTTTTTTTTTTTTTTTAGTAGAGACGGGGTTTCACCGTGTTAGCCAGGATGGTCT 84639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 TGAGCCACTGCGCCCAGCCGGTCTTTT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 CGAACTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCA 125
                                                                                                                                                                                                                                                                   sequence.
AC006137
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi; Mammalla; Entheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 129806)
Janer, M., Guillaudeux, T., Vu, Q., Kutyavin, T., Harter, H. and
                                                                                                                                                                                                                                                                                                                         AC006137 129806 bp DNA 1:
Homo sapiens clone SCb-254N2 (UWGC:rg254N02)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Wellcome Trust Sanger Institute Center code: SC
Geraghty, D.E.
                                                                                                                                                                                                                                       AC006137.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DAQB-36F16 is from a DNA-arts QBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/HGP/Chr6/MHC
                                                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGATCTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAATGCTGGGATTACAGGCG
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="DNA-arts-BAC.1-QBL.1"
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93.9%;
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Pred. No. 3.
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	REFERENCE AUTHORS TITLE JOURNAL
Sequence Validation: This sequence has been validated by Multiple Complete Digest Mapping. Comparison of the experimentally derived map digest fragments with sequence-predicted fragments is given below. Small fragments with sequence-predicted fragments given below. Small fragments with sequence-predicted fragments given below. Small fragments with sequence-predicted fragment groups are separated by dashed innes. HindIII Map Seq Map	Large scale sequence analysis of the human MHC class I region Unpublished Fred Hutchinson Cancer Research Center The Clinical Research Division 1100 Fairview Ave. N., P.O. Box 19024 Seattle, WA 98109-1024 2 (bases 1 to 129806) Geraghty, D.E. and Olson, M.V. Direct Submission Submitted (05-DEC-1998) Human Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA University of Washington Human Genome Center Box 352145, Seattle, WA 98195 Contact: Daniel E. Geraghty (geraghty@fhorc.org) 3 (bases 1 to 129806) Kaul, R.K. and Haugen, E.D. Direct Submission Submitted (24-AUG-2000) Genome Center, University of Washington, Box 352145, Seattle, WA 98195 USA University of Washington Genome Center Box 352145 Seattle, WA 98195 Contact: Rajinder Kaul (rkkaul@u.washington.edu) 4 (bases 1 to 129806) Kaul, R.K. and Haugen, E.D. Direct Submission Submission Scattle, WA 98195, USA On Oct 19, 2021 this sequence version replaced gi:9887710.

HS271M21/c HS271M21 134292 bp DNA linear PRI 14-SEP-2001 LOCUS HUMAN DNA sequence from clone RPI-271M21 on chromosome 6p21.31-22.2. Contains a MASI oncogene pseudogene, the OR2H2 gene for olfactory receptor 2H2, olfactory receptor 2H1 and 2H5 pseudogenes OR2H1 and DRSH5P, the gene for diubiquitin, an RPL13A (60S Ribosomal Protein L13A) pseudogene, the GRBBR1 gene for gamma-aminobutyric acid (CABA) B receptor 1 and an SMT3H1 or SMT3H2 (SMT3 (suppressor of mif two 3, yeast) homolog) pseudogene.	QY 126 TGAGCCACTGCGCCCAGCCGGTCTTTT 153	QY 66 CGAACTCCTGACCTCGTGATCCGCCCGCCTCCGGCCTCCCAAAGTGCTGGGATTACAGGCA 125	Qy 6 TITTTITTTTTTTTTTAGTAGAIGGGGTTTCACCGTGTTAGCCAGGATGGTCT 65	Query Match 15.4%; Score 133.6; DB 9; Length 129806; Best Local Similarity 93.9%; Pred. No. 3.2e-29; Matches 139; Conservative 0; Mismatches 9; Indels 0; Gaps 0;	l		/organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="6"	FEATURES Location/Qualifiers source 1129806	3796.27 3886.00	39 3681.	4322.0	2.48 910.0	2928.79 2931	տ :	7.00 3283.08 3301.0	1411.52 1408.00 2824.85 2828.00	5517.00 1708.46 1697	8.95 8430.00 4045.43 4133.00 6018.56	1461.00 4416.83 4379.00 754.07 745 	723.00 1182.00 1181.00 4157.75 4197.0	829.33 2792.00 2619.67	0 3764.58 3791.00 3143.81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality = 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. IMPORRANT: This sequence is not the entire insert of clone RP1-271M21 It may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for a 100 base overlap.

The true left end of clone RP1-271M21 is at 134292 in this sequence. The true right end of clone RP1-271M21 is at 1 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; TT:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        shorter because we sequence overlapping sections only once, except
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RP1-271M21 is from the library RPCI-1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On Jan 21, 2001 this sequence version replaced gi:4160199. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VECTOR: pCYPAC2
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SP; OR2IIP; RPL13A; SWT3H1; SWT3H2.
                                    8191.
                                                                                                                                                                                                               5815
sry1. .8565
/note="THEIC repeat: matches 1. .371 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                   note="HERV16 repeat: matches 596. .1091 of consensus"
                                                                                                                                                                                                                                                                                           note="MLT1C repeat: matches 17. .466 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
|mol_type="genomic DNA"
                                                             note="L1M4 repeat: matches 3415. .3586 of consensus"
                                                                                                                                                                          note="MIR repeat: matches 108. ,146 of consensus"
                                                                                                                                                                                                                                    'note="match: GSS: Em:AQ435929"
                                                                                                                                                                                                                                                                                                                                                     'note="MLT1A1 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                         note="MER94 repeat: matches 1. .134 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone_lib="RPCI-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="RP1-271M21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       map="p21.31-22.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome="6"
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      /note="SN5 repeat: matches 1. .235 of consensus" 30633. .30690
                                                                                           /note="match: GSS: Em:AQ195255
match: STS: Em:G61733"
                                                                                                                                                                                                                                                                /note="AluJb repeat: matches 1. .307 of consensus"
23272. .23353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MER4-internal repeat: matches 2198. .2701 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18234. .19882 /note="MER4-internal repeat: matches 2701. .4800 of consensus"
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/note="AluSx repeat: matches 2. .306 of consensus"
9002. .9354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MER4-internal repeat: matches 2341. .2464 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="AluJb repeat: matches 1. ,292 of consensus"
20182. ,20687
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/note="11MB6 repeat: matches 5767. .5786 of consensus"
                                                                                                                                                                                 note="MER4C repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                     'note="MER50 repeat: matches 1. .711 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                            consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="MER4-internal repeat: matches 121. .1037 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="LTR36 repeat: matches 1. .612 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="MER4-internal repeat: matches 1034. .1114 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'mote="match: GSS: Em:AQ743745"
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11386. .11537
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10027. .10047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="match: GSS: Em:AQ883063"
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DEFINITION
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                                                                   complete sequence.
AL662826
                                                                                                               Human DNA sequence from clone XXbac-101120 on chromosome 6,
Homo sapiens (human)
                                            AL662826.11 GI:20870241
                                                                                                                                      AL662826
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                                                                                                                                                                                                                                                     TGAGCCACCGCGCCCAGCCTTTTTTTT 113252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MLT1B repeat: matches 1. .374 of consensus" 37958. .38299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="dJ271M21.8
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complement(34169 ..35034)
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31856. .32461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="dJ271M21.8 (MAS1 oncogene pseudogene)
match: proteins: Sw:P30554 Sw:P12526 Sw:P04201 Sw:P35410"
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}5631. .35754
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33207. .33337
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 15.4%; Score 133.6; DB 9; Length 145431; Best Local Similarity 93.9%; Fred. No. 3.3e-29;
                                                                  ORGANISM
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humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On May 16, 2002 this sequence version replaced gi:20793440.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one MI3 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; Sw:,
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 TGAGCCACTGCGCCCAGCCGGTCTTTT 153
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                                                                                                                                                                                                                                                           Homo sapiens genomic DNA, chromosome 8, clone:RP11-139F9, complete
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                  Homo sapiens
                                                                                              Homo sapiens (human)
                                                                                                                                                                AP006245.1 GI:28812033
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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AL Submitted (23 ARR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger ac.uk Clone requests: clonerequest@sanger.ac.uk
On Mar 21, 2002 this sequence version replaced gi:19572047.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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Published Only in Database (2003)
2 (bases 1 to 15586)
Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T.
Totoki,Y., Watanabe,H. and Sakaki,Y.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="8"
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76.9%;
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67870 TGAGCCACCGCGCCCAGCCTTTTTTTT 67843
                                                                                                          67930 CGATCTCCTGACCTCGTGATCCGCCCCGCCTCGGCCTCCCAAAATGCTGGGATTACAGGCG 67871
                                               126 TGAGCCACTGCGCCCAGCCGGTCTTTT 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence was generated from part of bacterial clone contigs constructed by the MHC Haplotype Consortium and collaborators. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6/MHC.
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                                                                                                                                                                                                                                                                                                                                        Conservative
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/db_xref="taxon:9606"
/chromosome="6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="XXbac-126D10"
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RESULT 13 AC138080/c REFERENCE REFERENCE ORGANISM KEYWORDS VERSION DEFINITION ACCESSION Shoons AUTHORS TITLE AUTHORS JOURNAL Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Barra, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Charg, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Mathews, C., McCarthy, M., Melddrim, J., Meneus, L., Mihova, T., Mathews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Schauer, T., Terfave, S., Thankhang, T., Terfave, S., Thodany, T., Tonham, K., Terfave, S., Tengan, T., Terfave, S., Thodany, T., Tonham, K., Tengan, T., Terfave, S., Tengan, T., Ten 1 (bases 1 to 164872)
Birren, B., Nusbaum, C. and Lander, E. Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Unpublished Homo sapiens chromosome 8, clone RP11-1147M13 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiene Homo sapiens chromosome 8, clone RP11-1147M13, complete sequence. Homo sapiens (human) AC138080.4 GI:28565756 AC138080 (bases 1 to 164872) 164872 bp DNA linear PRI 26-FEB-2003

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family="	1 1		
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15877 16089	repeat_region	/orç	source
lement (15	repeat_region	Loca	FEATURES
1541315567 /rot family="(TTTC)n"	repeat_region		
AluJ/F	norfar_regin_	Center project intormation	
/rpt_family="AluSx"		ce submissions@g	
complement (1364213933)	repeat_region	Center code: WIBR Web site: http://www-seq.wi.mit.edu	
,,	repeat_region	Center: Whitehead Institute/ MIT Center for Genome Research	
complement(1316813252) /rpt family="MIR"	repeat_region	http://ftp.genome.washington.edu/RM/RepeatMasker.html	
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1133311463	repeat_region	Submitted (26-FES-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	JOURNAL
complement (1081211181)	repeat_region		TITLE
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MIR	+ 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,	
/rpt_family="FRAM"		Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C.,	
-	repeat_region	Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,	
85578798 /rot family="MIR"	repeat_region	Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,	
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/rpt_ramily="(CATA)n" complement(8072845	repeat region	<pre>Lindblad-Toh.K., Liu,G., Lui,A., Mabbitt,R., MacLean,C., Macdonald.p. Major.J. Manning.J. Matthews.C. McCarthy.M.</pre>	
80228069	repeat_region	Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,	
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/rot family="MIR3"	repeat_region	Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,	AUTHORS
т		4 (bases 1 to 164872)	REFERENCE
57136040	repeat region	Submitted (15-JAN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	JOURNAL
complement (50015111)	repeat_region	Direct Submission	TITLE
/rpt family="AluJb"	Torbed Transfer	Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wwman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A., and Zody,M.	
Ηh	 - -	Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K.,	
45264549	repeat_region	Seaman.S., Severy.P., Smith.C., Spencer.B., Stange-Thomann.N.,	
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_family="(CA)		<pre>Miconga, v., Murpny, Y., Maylor, J., Mguyen, C., Micol, K., Morbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J.,</pre>	
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37794068	repeat_region	Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,K., Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J.,	
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<pre>/rpt family="MLT1J"</pre>	repeat_region	<pre>Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna.S. Gord.S. Graham L. Grand-Pierre,N. Hafez,N.</pre>	
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complement (20252158)	repeat_region	<pre>Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,</pre>	AUTHORS
f . 18	repeat_region	esearch, 3	JOURNAL
15091629	repeat_region	Direct Submission	TITLE
/rpt_family="AluJo"	repear_region	<pre>Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.</pre>	

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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
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                                                                                                                                                                                                                                                                                                                                AUTHORS
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Nuzry, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, B., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Dugan-Rocha, S., Durbin, K.J., Earnbart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabist, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11921 CTAACATGTGGGATATCTCACCATTGGTCAAA 11890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11981 ACCACGCCCGGCCTACATTTTTCATGATGCATAGGGCAAGAAAAGTTGAACACTTGTAAC 11922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12041 CCTGACCTCGTGATCCGCCCGCCTCAGCCTCCCAAAGTGTTGGGATTACAGGCGTGAGCC 11982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12101 TITTITIGIATITITAGIAGAGACGGGGTTTCACCGTGTTAGCCAGGATGGTCTCCATCT 12042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 ACTGCGCCCAGCCGGTCTTTTAAACATTCCCCAGGACTGTACAGCCAACCCATACTCAC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192 CTGACATTTGGGAACTCCCCCCACGGCCATA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 TITTTTTTTTTTAAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATGGTCTCGAACT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 CCTGACCTCGTGATCCGGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCC 131
                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 199706)
                                                                                                                                                                                                                                                                                                                                                                                                                            HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP. Pan troglodytes (chimpanzee)
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199706 bp DNA linear HTG 20-OK
Pan troglodytes clone RP43-45G20, WORKING DRAFT SEQUENCE, 10
unordered pieces.
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17680. .18076
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20487. .20666
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18402
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18317 .18351
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T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        family="HAL1"
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Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hollins, B., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L. B., Jacobson, B., Jia, Y., Johnson, R., Lewis, L.C., Karlston, E., Kelly, S., Khan, U., King, L., Korvah, J., Lewis, L.C., Liu, J., Liu, J., Liu, Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, M., Lewis, L.C., Lewis, L., Lozado, R.J., Lucier, A., Lucier, R., Marding, R., Morgan, M., Martinez, R., Martinez, R., Martinez, R., Martinez, R., Lucier, R., Martinez, R., Lucier, R., Martinez, R., Martinez, R., Martinez, R., Martinez, R., Martinez, R., Martinez, R., Wall, R., Mashington, C., Walliams, G., Williams, A., Wilczyk, R., Wooden, S., Weinstock, G. and Gibbs, R., Wall, Y., F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (14-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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Sequencing vector: Plasmid; M77789

Sequencing vector: Plasmid; M77789

Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329

Consensus quality: 195498 bases at least Q40

Consensus quality: 201324 bases at least Q20

Consensus quality: 206344 bases at least Q20

Consensus quality: 206344 bases at least Q20

Consensus quality: 206344 bases; as least Q20

Setimated insert size: 207444; sum-of-contigs estimation

Quality coverage: 0x in Q20 bases; sum-of-contigs estimation

Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: ZUAO
Center clone name: RP43-45G20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: hgsc-helpsbcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.hgsc.bcm.tmc.edu/
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REFERENCE

JOURNAL TITLE

COMMENT

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* NOTE: Bstimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 10 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                             102376
102476
115012
115112
139606
                                                  139706
                                                                                                                                                                                                                   47629
47729
                                                                                                                                                                                                             47628: contig of 47628 bp in length
47728: gap of unknown length
102375: contig of 54647 bp in length
139705: gap of unknown length
160888: contig of 21153 bp in length
160958: gap of unknown length
169439: contig of 8481 bp in length
                                                                                                           115111: gap of 
139605: contig
                                                                                                                                                             102475: gap of
115011: contig
                                                                                                           unknown length
of 24494 bp in length
                                                                                                                                                                   of 12536 bp in length
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FEATURES
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102815 GTCTCGATCTCCTGAACTTGTGATCCACCCGCCTCGGCCTCTCAAAGTGCTGGGATTACA 102874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102755 CTAATTTTTTTTTTTTTTTTTTAGTAGAGACGGGGTTTCACCGTGTTAGCCAGGATG 102814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 GGCATGAGCCACTGCGCCCAGCCGGTCTTTTTAAACATTCCCCAGGACTGTA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 GTCTCGAACTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACA 121
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                                                                                                                                                          Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 31% of reads Chemistry:
Dye-terminator Big Dye; 68% of reads
Consensus quality: 202124 bases at least Q40
Consensus quality: 204084 bases at least Q30
Consensus quality: 204084 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Cione colonerequestesanger.ac.uk
On Sep 9, 2000 this sequence version replaced gi:9926590.
                                                                                       Insert size: 206562; sum-of-contigs
Insert size: 201559; 10.0% error; agarose-fp
Quality coverage: 5.18x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL355484 10-JUL-3 DNA linear HTG 10-JUL-3 Homo sapiens chromosome 1 clone RP11-370E21, 9 unordered pieces
                                                                                                                                                                                                                                                                                                                                                                                     Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Sanger Centre
Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL355484.10 GI:10039826
HTG; HTGS_PHASB1; HTGS_CANCELLED.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL355484
                                                                        coverage: 5.38x in Q20 bases; agarose-tp
                                                                                                                                                                                                                                                                                                                                                           Center project name: bA370E21
                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: SC
Web site: http://www.sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
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182344: contrig of 12805 bp in length
182444: gap of unknown length
190235: contrig of 7791 bp in length
190335: gap of unknown length
196363: contrig of 6328 bp in length
196763: gap of unknown length
199706: contrig of 2943 bp in length
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Pred. No. 3.3e-29;
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                             72 CCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCC
                                                                                           12 TTTTTTTTTTTTAGGTAGAGATGGGGTTTGACCGTGTTAGGCAGGATGGTCTCGAACT 71
                                                                                                                                             163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                 Similarity
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fragment_chain:1"
                                                                                                                                                                                                                                                          clone end:SP6
                                                                                                                                                                                                                                                                                                             fragment_chain:
131361. .207362
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127654. .131260
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fragment_chain:2
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fragment_chain:2"
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fragment_chain:2"
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fragment_chain:1"
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fragment_chain:1"
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fragment_chain:1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                     note="assembly_fragment:00004"
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127653: gap of 100 bp
131260: contig of 3607 bp in length
131360: gap of 100 bp
207362: contig of 76002 bp in length
                                                                                                                                                               15.4%;
76.9%;
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20103:
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2: gap of 100 bp
3: contig of 1971 bp in length
3: gap of 100 bp
3: gap of 100 bp in length
3: gap of 100 bp in length
6: gap of 100 bp
9: contig of 26221 bp in length
9: gap of 100 bp
9: gap of 100 bp
1: contig of 4632 bp in length
1: gap of 100 bp
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contig of 50332 bp in length
gap of 100 bp
                                                                                                                                             0; Mismatches
                                                                                                                                                             Score 133.6; DB 2;
Pred. No. 3.3e-29;
                                                                                                                                                 49;
                                                                                                                                                 Indels
                                                                                                                                                                                    Length 207362;
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Search completed: May 24, 2004, 15:09:30 Job time: 2506 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Database : Title: Perfect score: Post-processing: Listing first 45 summaries Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Total number of hits satisfying chosen parameters: Word size : Searched: Scoring table: Sequence: Run on: OM nucleic - nucleic search, using sw model May 24, 2004, 15:50:42; Search time 2500 Seconds (without alignments) 15031.364 Million cell updates/sec OLIGO_NUC Gapop 60.0 , Gapext 60.0 US-10-621-363-12
867
1 togagttttttttttttttt.....accaatctcgtgccgaattc 867 3470272 seqs, 21671516995 residues GenEmbl: * gb htg. em_ro:*
em_sts:*
em_un:*
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em_htg_hum:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C026298 Homo s	08007	121247 Homo sap	51663 HOMO 8	L35935 Human UN	UZ/62 HOMO S	0984/6 HOMO 8	CODY HOMO	OCCUPATION OF	067823 Homo s	297357 Homo s	567	121893 Human	6377 Human	026552 Homo sap	024472 Homo E	C145421 Homo sap	C108112 Homo sap	C004935 Homo sap	P001752 Homo sap	135048 Homo sap	132806 ното вар	01052 Homo sap	Cl38417 Homo sap	02056 Ното вар	Y055360 Homo sap	P001692 Homo sap	7885 Homo sap	11982 Homo s	005076 Homo sap	001342 Homo sap	355146 Human DN	683807 Human	683875 Homo sap	20890 Homo sap	004840 Homo s	004537 Homo sap	021026 Homo sap	000050 Pan trog	0154	37041 9	16 Se	634 Seque	7 Sequen	AK095438 Homo sapi	L031296 Human DN	Description

ALIGNMENTS

TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	HS888M10/c	RESULT 1
Direct Submission	Cobley, V.	1 (bases i to 124874)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	Homo sapiens (human)	HTG.	AL031296.1 GI:4106564	AL031296	1p36.11-36.31, complete sequence.	Human DNA sequence from clone RP5-888M10 on chromosome	HS888M10 124874 bp DNA linear PRI 04-MAR-2003		

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw:, SWISSPROT; Tr:, TREMEL; Wp:, WORMPEP; Information on the WORMPEP database can be found at the tp://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chri
RP5-888M10 is from the library RPGI-5 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
87225 CGAACTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCA
                                                                                                                                                                                                                                                                                                                                                                                          87285 TTTTTTTTTTTTTTTTTAAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATGGTCT 87226
                                                                                                                                                                                                                       126 TGAGCCACTGCGCCCAGCCGTCTTTTAAAACATTCCCCAGGACTGTACAGCCAACCCAT 185
                                                                                                                                            186 ACTCACCTGACATTTGGGAACTCCCCCCCCCCATAACTGATCTGCAGAGGTAAGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jan 5, 1999 this sequence version replaced gi:3881974.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 55.7%;
Similarity 99.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="RZPD:RPCIP704M10888"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ninomiya, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T., Kodaira, H., Furuya, T., Takahashi, M., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, M., Sato, K., Tanikawa, M., Yamazaki, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamorto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kimura, K., Yamashita, H., Matsuo, K., Nakamara, Y., Sekine, M., Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
Direct Submission
Submitted (04-UUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Ramatari, Kisarrazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
MEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one passe sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and
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                        87 CGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGC 124
                                                                                   27 AGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATGGTCTCGAACTCCTGACCTCGTGATC 86
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Patent: W
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Cancer gene determination and therapeutic screening using signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 646 from Patent W00194629.
                                                                                                                                                                                                                                                                                                                                                          Avalon Pharmaceuticals
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Conservative
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/mol type="mRNA"
/db xref="taxon:9606"
/clome="DJOST2004637"
/cell_type="CD34+ cells"
                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/note="cloning vector: pME18SFE3~mRNA from CD34+ cells
after 3-days ODF induction.~primary culture, CD34+ Cells"
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                                                                                                                                                                11.3%; Score 98; DB 6; Length 145831; 100.0%; Pred. No. 6.4e-46;
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                                                                                                                                               0; Mismatches
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z.
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AX336416
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Cancer gene determination and therapeutic screening using signature
                                                                                                                                                                                                                                                                                Patent: WO 0194629-A 6925 13-DEC-2001;
                                                                                                                                                                                                                                                                                                                  Cancer gene determination and therapeutic screening using signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
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Location/Qualifiers
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AX334634
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ilarity 100.0%; Pred. No. 6.4e-46;
Conservative 0; Mismatches 0;
                                                                         Conservative
                                                                                                                                                             /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
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                                                                       11.3%; Score 98; DB 6; I
100.0%; Pred. No. 6.4e-46;
vative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                        Mammaila; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 14531)

Loftus, B.J., Kim, U.J., Sneddon, V.P., Kalush, F., Brandon, R., Fuhrmann, J., Mason, T., Crosby, M.L., Barnstead, M., Cronin, L., Deslattes Mays, A., Cao, Y., Xu, R.X., Kang, H.L., Mitchell, S., Bichler, E.E., Harris, P.C., Venter, J.C. and Adams, M.D. Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q genomics 60 (3), 295-308 (1999)
                            Submitted (29-APR-1997) The Institute for Genomic Research, Medical Center Dr., Rockville, MD 20850, USA 3 (bases 1 to 145831)
Adams,M.D. and Loftus,B.J.
Direct Submission
                                                                                                                                                                                        Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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NC clone CIT9875K-A-815A9, complete sequence.
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ent WO0194629.
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BAC Clone CIT987SK-815A9 is located in chromsome 16. Genes
were identified by a combination of five methods: XGRAIL (available
by anonymous ftp from arthur.epm.ornl.gov), Genefinder (available
by anonymous ftp from colin@u.washington.edu), GENSCAN (available
using the e-mail server at genscan@gnomic.stanford.edu), searches
of the BST database at TIGR (http://www.tigr.org/tdb/hod/hod.hrml)
and searches against a peptide database. Repeats were identified
using RepeatMasker (Smit, A.F.A. and Green, P. unpublished,
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Location/Qualifiers
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FIDEGLIQPOI ELI ERENNE PERULLALERENWEKATIKS PVELLARASIDKEVADLAKUVA
PKOLKOKTERSI IHYAGKVU YNASAMLIKNOD PLINDWTSLLARASIDKEVADLAKUVA
RI VGLIDQMAKMTESSLES ASKITKKGMPET TVGOLYKEQLIGKLAMISIDKEVADLAKUVA
RI VGLIDQMAKMTESSLES ASKITKKGMPET TVGOLYKEQLIGKLAMIT LRINTEPIPEVRCI IP
RHEKRSGKLDAFLVLEQLECNEVLEGIR I CRQGEPIRE I VFQEFER KYELIAANAL PKG
PMOGKQACILIMI KALELDPRILYRI GOSKI FPETGVLLAHLEEBRDLKITDVI MAPQAKC
RGYLLARAFAKRQQQLTAMKVI QRICAAYLKLIRAWQMEDLETKVEPLLQVTRQEEBRVAL
AKKQELESI LHEMEARLEBEDGLQRISQLTBEKKMLLQBQLQABATELYARAEBRANILYRL
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EKVITABAKI KKLEDBEL I VMDDQNIKLI SKERKLLEBGRISDFHEQLADLAQAQI AELKKQLAK
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BELBALKTELBDTLOSTATQDELRKLKKTLEGDASDFHEQLADLAQAQI AELKKQLAK
KEBBLQAALARLDDEI AQNINALKKI RELEGHI SDLQEDLDSERAARINKAEKQKRDLG
BELBALKTELBDTLOSTATQDELRKLKKRLEGADASDFHEQLADLAGAI KLAKDVASLSSQLQD
TQBLLQBETROKLAVSTKLAQLEBERNSLODDLDERBERAKGARDKASLSSQLQD
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TQBLLQBETROKLAVSTKLAQLEBERNSLODDLDERBERAKGALKTENISTINI OLSDISK
KKLODES AGKTONDA TKLARDEBERNSLODDLDERBERAKGALKTENISTINI OLSDISK
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53885...53948,56552...56650,61016...61159,68837...68932,
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117456...117564,117647...117819,128605...128737)
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LLQANPILEAFGNAKTVKNDNSSRFGKFIR INFDVTGIVGANIETYLLEKSRAIRQA
RDERIFHIFYMIAGAKEMRSDLLLEGFNNYFLSNGFYPIFAAQDDEMFQETVEA
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QGASFLGILDIAGFEIFEVNSFBQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEMN
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/mol_type="genomic DNA"
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and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattorl@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
                                                               Hattori,M., Toyoda,A., Watanabe,H., Taylor,T.D., Kuroki,Y., Fujlyama,A. and Sakaki,Y.
Direct Submission
Direct Submission
Submitted (12-MAY-2003) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                             The Chimpanzee Chromosome 22 Sequencing Consc DNA sequence of chimpanzee chromosome 22 and
                                                                                                                                                                                                                                                                                                                                                                                                                               BS000050
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EDELQATEDAKLRLEVINKQALKOOFERDLQARDEQNEEKRROLQRQLHEYETELEDER
KQRALAAAKKKLEGDLKDLELQADSALKOOFERDLEVERTEKORDLEKGELESELSGRN
KQRALAAAKKKLEGDLKDLELQADSALGABAEAIKQLRLGKEELAEELASSLSGRN
RDEIFATAKENEKKAKSLEADLKVOLGEDLAABERARKQADLEKEELAEELASSLSGRN
ALQDEKERLEARIAQLEEELEEDGONMEAMSDRVRKATQQAEQLSNELATERSTAQKN
ESARQOLERQNKELRSKLHEMEGAVKSKFKSTIAALEAKIAQLEEQVEQEAREKQADLANT
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RRKLQRELDEATESNEAMGREVNALKSKLRRGNETSFVPSRRSGGRRVIENADGSEEE
                                                                                                                                                                                                                                                                                             Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="A-815A9.1"
/db_xref="dbSTS:G13593"
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'db_xref="dbSTS:G;
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/db_xref="dhs=s-7"
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/db_xref="dhcmo"
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/db_xref="dbsqs.c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _xref="dbSTS:Z16518"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone:RP43-038C12, map
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The CHORI-251 chimpanzee BAC library was prepared from DNA isolated from the blood of a single male chimpanzee using published protocols (Osoegawa, K. et al. Genomics 52:1-8). The DNA from the chimpanzee ('Clint') was obtained from the Yerkes Primate Center in Atlanta. The library was prepared by Baoli Znu, Chung Li Shu, Kazuttyy Osoegawa, Evan Eichler & Pieter J de Jong. The library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Source information:
The RPCI-43 chimpanzee BAC library was prepared from DNA isolated from the blood of a single male chimpanzee using published protocols (Osoegawa, K. et al. Genomics 52:1-8). The DNA from the chimpanzee ('Clint') was obtained from the Yerkes Primate Center in Atlanta. The library was prepared by Baoli Zhu, Chung Li Shu, Kazutoyo Osoegawa, Evan Eichler & Pieter J de Jong. The library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            characteristics are described at
http://www.chori.org/bacpac/mchimp43.htm.
The clone may be obtained from Pieter J. de Jong and coworkers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: pUC18,pUC13,pTZ19R; 100% of reads Chemistry: Dye-terminator Big Dye and ET; 100% of reads Assembly program: Phrap; version 0.990329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel:81-45-503-9111, Fax:81-45-503-9170)
The Chimpansee Chromosome 22 Sequencing Comsortium consists of:
The Chimpansee Chromosome 22 Sequencing Comsortium consists of:
*Chinese National Human Genome Center at Shanghai, Shanghai, China
*GBF, Dept. of Genome Analysis, Braunschweig, Germany; *Institute
of Molecular Biotechnology, Jena, Germany; *KRIBB Genome Research
                                                                                                              chimpanzee.
                                                                                                                                                                                                                                                                                                                                              chimpanzee.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.chori.org/bacpac/chimpanzee251.htm.
The clone may be obtained from Pieter J. de Jo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      an attempt was made to resolve all sequencing problems, a compressions and repeats; all regions were covered by at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Consensus quality:
                                                                             Clones may be obtained from Asao Fujiyama and co-workers
                                                                                                                                                                                           The PTF22 chimpanzee Posmid library was prepared from DNA isolated
                                                                                                                                                                                                                                                                                                         Clones may be obtained from Asao Fujiyama and co-workers
                                                                                                                                                                                                                                                                                                                                                                                      cultured cells established from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              characteristics are described at
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Consensus quality:
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Contact: hattori@gsc.riken.go.jp
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*Max-Planck-Institute for Molecular Genetics, Berlin, Germany;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (http://www.chori.org/bacpac).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (http://www.chori.org/bacpac)
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                                    http://www.gsc.riken.go.jp)
                                                                                                                                                          rom cultured cells established from the blood of a single male
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                                                                                                                                                                                                                                pKS145
                                                                                                                                                                                                                                                                                                                                                                                  chimpanzee BAC library was prepared from DNA isolated from cells established from the blood of a single male
pKS143
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                                                                                                                                                                                                                                                                gsc.riken.go.jp).
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primatees; Catarrhini; Hominidae; Homo.

RCE 1 (bases 1 to 75555)

RS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bomin,D., Bouck,J., Bowie,S., Brieva,M., Brown,B., Brown,M., Bryant,N.P., Bouck,J., Bowie,S., Brieva,M., Brown,B., Brown,M., Bryant,N.P., Bouck,J., Charler,M., Carvazos,S.R., Chacko,J., Chavez,D., Charler,M., Carvazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Carter,M., Cavazos,S.R., David,R., David,R., David,R., David,R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., David,R., David,R., David,R., David,R., David,R., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Deuthwaite,K.J., Draper,H., Dugan-Rooha,S., Durbin,K.J., Frantz,P., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Garza,N., Gill,R., Gorrell,J.H., Guevara,M., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,M., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,M., Garner,T., Hawes,A., He,X., Harris,R., Hogues,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Holler,S., Hame,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Mallyk,S., Hume,J., Luxis,B., Levis,B., C., Lichtarge,O., Lieu,C., Liu,M., Lucler,R., Luna,R., Martin,R., Martindale,A., Martindale,A., Mooris,S., Moser,M., Moalabat,K., Mooris,S., Moser,M., Neal,D., Neatson,J., Newtson,N., Nguyen,A., Nguyen,N., Nguyen,N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75555 bp DNA linear PRI 29-JUL-20
Homo sapiens 3 BAC RP11-85A3 (Roswell Park Cancer Institute Human
BAC Library) complete sequence.
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/db_xref="taxon:9598"
/chromosome="22"
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/clone_lib="RPCI-43 chimpanzee BAC"
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                         Submitted (29-JUL-2002) Human Genome Sequencing Center, Depayor Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA On Jul 29, 2002 this sequence version replaced gi:21747431. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                        Submitted (14-JUL-2002) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (12-JAN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 75555)
gc-help@bcm.tmc.edu
                                                                                                                                                                                                             Direct Submission
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TITLE

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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and

local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found

http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht

Location/Qualifiers

FEATURES Source

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Homo sapiens PAC clone RP5-872F7 from 7, complete sequence
ACO04537
                                                                                                                                                                                                                                                            Direct Submission
Submitted (09-APR-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
4 (bases 1 to 88872)
                                                                                                                                                                                                                                                                                                                             3 (bases 1 to 88872) Waterston, R.
                                                                                                                                                                Wilson, R.
                                                                                                                                                                             Submitted (03-FBB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA (bases 1 to 88872)
                                                                                                                                                                                                                                Waterston, R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                               Unpublished (2001)
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The sequence of Homo sapiens PAC clone RPS-872F7
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Suiston, J.B. and Wilson, R.
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              Web site: http://genome.wustl.edu
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_DJ0872F07
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/function="unresolved tandem repeat"
15712. .15897
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1571I .15899
'note="size confirmed by restriction map, formally
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14062. .14090
/rpt_family="(A)n"
complement(14254. .14312)
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14887. .14916
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100.0%; Pred. No. 1.3e-40;
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complement(10400...10697)
/rpt family="AluJb"
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family="AluJb"

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' 'Dt family="AluJo" 10037. 1000"

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ily="HAL1"

/rpt_family="AluJb"
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.2600)

_family="AluSq"

/rpt_family="AluJo" complement(475. .65)

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_family="MIR"

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/clone="RP11-85A3"

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family="AluSq" [ement(190. .474)

/mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="3"

repeat_region repeat_region

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family="L1MB4"

/rpt_family="L1MB4" complement (13378. ...

family="MSTB"

/rpt 13257 /rpt_f: 12955.

family="AluY"

/rpt_family="L1MB4"
complement(12797. .12831)
/rpt_family="U2"

_family="L1MB4"

/rpt_t 12350.

_family="AluSq"

/rpt_family="L1MB4" 12037. .12349

/rpt 11872

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone was derived from human PAC library RPCI-4, prepared by Pieter de Jong and coworkers at http://www.chori.org using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor.

The clone may be obtained either from Genome Systems, Inc. (http://www.genomesystems.com) or Research Genetics, Inc. (http://www.resgen.com); or from Pieter de Jong.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov/or see http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone settions once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE INFORMATION:
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  /rpt_family="AcHobo"
8973. .9747
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7760. .8206
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/db_xref="taxon:9606"
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9856. .10618
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                                                                                                                       Submitted (09-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6: On Mar 9, 2002 this sequence version replaced gi:10716623.
                                                                                                                                                                                                                                   University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA 5 (bases 1 to 149397)
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Edwards,J., Wollam,A., Walker,C., Gregory,S., Hawkins,M. and Fiedler,T.
                                                                                                                                                                                                                                                                                                                                         MO 63108, USA
4 (bases 1 to 149397)
                                                                                                                                                                                                                                                                                                                                                                                  Submitted (12-JUN-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence of Homo mapiens PAC clone RP4-607J2 Unpublished (2001)
                                                                                                                                                                                                     Direct Submission
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Homo sapiens PAC clone RP4-607J2 from 7, complete sequence.
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Center project name: H_DJ0607J02
                                                                                 Center: Washington University Genome Sequencing Center Center code: WUGSC
                                          Contact: sapiens@watson.wustl.edu
                                                         Web site: http://genome.wustl.edu/gsc
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47662. .47758,49546. .49617,50449. .50568,50854. .51011,
51931. .52124,53608. .53800,56125. .56163,57648. .58210)
/gene="ING3"
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33669__33695
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                       Summary Statistics
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest. This sequence was finished as follows unless otherwise noted:

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Bric D. Green, Director), John D. McPherson in the Department of Genetics (Mashington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DLR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

묽 Ś 밁 á

This clone was derived from human PAC library RPCI-4, prepared by Pieter de Jong and coworkers at http://www.chori.org using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994) The library is from one male donor. {1994}.

The clone may be obtained either from Genome Systems, Inc. (http://www.genomesystems.com) or Research Genetics, Inc. (http://www.resgen.com); or from Pieter de Jong. VECTOR: pCYPAC2

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP5-1125K23, 200 bp overlap. Actual start of this clone is at base position 1 of RP4-607J2; actual end is at base position 149397 of RP4-607J2.

There are polymorphic base changes between RP4-607J2 and CTD-2312I3. The sequence RP4-607J2 contains an unresolvable tandem repeat from base position 21064 to 22995 whose sequence fidelity can not be guaranteed. Digest information suggests that there are 82 bases missing in the sequence.

FEATURES repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region Bource /rpt_family="MIR" 6966. .7279 /rpt_family="MER1_type" 5780, .5847 /rpt_family="MIR" 3423. .3491 /rpt_family="Alu" 7592. .7680 /rpt_family="MaLR" 7280. .7591 /rpt_famil rpt_family="G-rich" /clone_lib="RPCI-4" /mol_type="genomic DN /db_xref="taxon:9606" rpt_family="MER1_type" 'rpt_family="(TCCA)n" clone="RP4-607J2" organism="Homo sapiens" chromosome=#7" .149397 y="MIR"

repeat_region

/rpt_family="MaLR' 8860. 8880

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misc_feature
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/rpt_family="MER1_type"
27883. .28182
/rpt_family="Alu"
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23315. .2340c
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21653. .21754
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12747, .13000
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Macuty, L.M., Addmis, C., Addo-Occucia, H., All-Smanl, F.K., Allebrooks, S.L., Amarattinge, H.C., Are, J.R., Ayele, M., Barks, T., Barbaria, J., Benton, J., Binage, K., Blankenurg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, B., Brown, M., Bryant, N.P., Blankenurg, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, R., David, R.L., Davis, C., Dayer, H., Dugan-Rocha, S., Durbin, H.H., Delanney, K.R., Delgado, D., Denn, A.L., Ding, Y., Dinh, H.H., Delanney, K.R., Delgado, D., Denn, A.L., Ding, Y., Dinh, H.H., Delanney, K.R., Delgado, D., Denn, A.L., Ding, Y., Dinh, H.H., Delanney, K.R., Degar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earthart, C., Edgar, D., Edwards, C.C., Ding, Y., Dinh, H.H., Delanney, K.R., Delgado, D., Denn, A.L., Ding, Y., Dinh, H.H., Delanney, K.R., Delgado, D., Denn, A.L., Ding, Y., Dinh, H.H., Delanney, K.R., Delgado, D., Denn, A.L., Ding, Y., Dinh, H.H., Delanney, K.R., Delgado, D., Denn, A.L., Ding, Y., Dinh, H.H., Dilloway, C., Falls, F., Ferantz, P., Frantz, P., Falls, F., Ferantz, P., Falls, F., Ferantz, P., Falls, F., Ferantz, P., Falls, F., Ferantz, P., Garria, R., Garner, T., Garza, N., Gill, R., Garria, R., Garza, N., Gill, R., Garria, R., Garria, R., Garza, N., Gill, R., Garria, R., Garza, M., Gill, R., Garza, N., Gill, R., Garza, M., Garza
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Homo sapiens 3 BAC RP11-79L9 (Roswell Park Cancer Institute Human
BAC Library) complete sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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28544. .2861"
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28252. .28543
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standards - estimated error rate less than 1 per 10,000 bases.
Reports of lowest quality individual bases and measures of base
quality are listed below. Description of the metrics can be found

at URL:

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SEQUENCING READ COVERAGE. Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
                                                                                                                                                                                                                                                                            unpublished.) for Human and Mouse sequences.

Gennes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, Repeats are identified using RepeatMasker)
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Direct S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLOWE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the gequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (15-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jun 25, 2002 this sequence version replaced gi:21328480. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
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                                                                                                                                                                                                                                                      identical matches are annotated as similar.
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COMMENT

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality

PEATURES repeat_region misc_teature Bource repeat_region http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht complement (11032. .11705) complement (10761 /rpt_tamily="HAL complement(9770. complement (9727. /rpt_family="Alu.complement(8877. /rpt_tamily="L1M4"
complement(8413. .8509) /rpt_family="(TAAA)n"
complement(7599. .768 7326 . 744L /rpt_famil /rpt_family="AT_rich"
complement(6403. .670 /rpt_family="AT_rich"
complement(3409. .371; complement (9388 complement (8536. complement(633...930)
/rpt_family="AluSx" rpt_family="(TAA)n" complement (324. Location/Qualifiers rpt_family="AluJb" rpt_family="AluJb" rpt_family="T-rich" rpt_family="MIR" function="clone overlap" 'mol_type="genomic DN 'db_xref="taxon:9606" clone="RP11-79L9" organism="Homo sapiens" note="overlaps bases 109101. .111104 of clone AC117389" chromosome="3" .2004 _family="HAL1" _family="Alusg" _family="AluJb" _family="LIM4" family="AluSq" _family="AluSx" family="L1MB8" family="AluSq" family="Alusx" family="L1MB8" family="AluSp" family="AluJo" family="AluJo/FRAM" family="L1M4" family="AluSx" family="(TTTG)n" family="HAL1" family="AluSx" Y="FLAM_C" . 628) .10778) .9170) .9427) .8149) .1647) .9760) .7682) .8794) .11041) 7946) 3712)

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Chemistry: Dye-terminator Big Dye; 13% of reads
Chemistry: Dye-terminator Big Dye; 13% of reads
Consensus quality: 182378 bases at least Q40
Consensus quality: 183293 bases at least Q30
Consensus quality: 183854 bases at least Q20
Insert size: 184527; sum-of-contigs
Insert size: 179006; 2.7% error; agarose-fp
Quality coverage: 9.16x in Q20 bases; sum-of-contigs Quality
coverage: 10.59x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-APR-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. B-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Apr 2, 2003 this sequence version replaced gi:28971596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens chromosome X clone RP11-446K8, 5 unordered pieces. AL683875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: humquery@sanger.ac.uk
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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complement(11729. .12011)
/rpt_family="Alu8x"
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11706. .11728
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49340: contig of 49340 bp in length
49440: gap of 100 bp
91479: contig of 42039 bp in length
91579: gap of 100 bp
94862: contig of 3283 bp in length
94962: gap of 100 bp
119846: contig of 24884 bp in length
119946: gap of 100 bp
184927: contig of 64981 bp in length
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:. EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
                                                                                                                                                                                                                                                                                                                                                                         Submitted (22-NOV-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Nov 24, 2002 this sequence version replaced gi:24474461.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 189825)
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                                                                                                                                                                                                                                                                               Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                     Web site:
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119947. .184927
/note=masembly_fragment:04655
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94963. .119846
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49441. .91479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91580. .94862
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .49340
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/chromosome="X"
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                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .184927
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om clone RP13-297E16 on chromosome
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AL Submitted (19-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, UK. B-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest&sanger.ac.uk clone requests: clonerequest&sanger.ac.uk clone buring sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw. SWISSPROY, Tr. TREME; Wp:, WORMPEP, Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 57447)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human DNA sequence from clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/ChrX
RP13-297E16 is from the library RPCI-13.2 constructed by the group of Pieter de Jong. For further details see
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/db_xref="taxon:9606"
/chromosome="X"
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RPII-31101 is from the library RPGI-11.2 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMPORTANT: This sequence is not the entire insert of clone RP11-31101 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-31101 is at 1 in this sequence true left end of clone RP11-135M8 is at 57348 in this sequence. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="LIME2 repeat: matches 5812. .6002 of consensus" 6774. .7192
                               24575. .24903
                                                                                                                                                                                                            complement (15388.
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/note="LIPA16 repeat: matches 5783. .6149 of consensus"
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/note="MEE91 repeat: matches 100. .124 of consensus"
                                                                                   /note="24 copies 2 mer ca 72% conserved"
18406. .24551
                                                                                                                                                                                                                               /note="AluJ/FRAM repeat: matches 232, .293 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                   8755. .8938
/note="MIR repeat: matches 58. .245 of consensus"
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1336. .1506
                                                       'note="L1PA3 repeat: matches 3. .6146 of consensus"
                                                                                                                                                                       note="match: GSS: Em:AQ719416"
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/note="Ll repeat: matches 3631. .4476 of consensus"
note="MER58B repeat: matches 1.
                                                                                                                                                                                                                                                                                          note="MLT1F repeat: matches 360. .533 of consensus"
                                                                                                                                                                                                                                                                                                                                                  'note="MIR repeat: matches 24. .262 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="L1M4 repeat: matches 2670. .3000 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="L1ME2 repeat: matches 4962. .5246 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="L1ME2 repeat: matches 5312. .5763 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="L2 repeat: matches 2492. .2750 of consensus"
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/chromosome="6"
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                                                                                                                                              .15613
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   .341 of consensus"
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/44378. .44457
                                                                                                                                                                                                      /note="match: GSS: Em:AQ059083"
48788. .49089
                                                                                                                                                                                                                                                   /note="L2 repeat: matches 2005. .2286 of consensus"
complement(47915. .48258)
                   /note="MLT2CB repeat: matches 1. .501 of consensus"
49999. .50436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="L1PA4 repeat: matches 4645. .6146 of consensus"
43305. .43385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35045. .35108
/note="L1ME3 repeat: matches 5891. .5951 of consensus"
35119. .35267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="L1MB6 repeat: matches 5938. .6108 of consensus" complement (31361. .31864) /note="match: GSS: Em:AQ120459"
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27440. .27491
/note="L1MC4 repeat: matches 6655. .7093 of consensus"
                                                                                                                                                                                                                                                                                                  /note="L2 repeat: matches 2629. .2709 of consensus"
44718. .44985
                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="LiPA16 repeat: matches 5287. ,5375 of consensus"
43386. .44026
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41699, .43199
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35593, .35780
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                                                                                      note="L1MC4 repeat: matches 6477. .6655 of consensus"
                                                                                                                                   'note="104 copies 2 mer aa 76% conserved"
                                                                                                                                                                             note="Alusx repeat: matches 5. .305 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                               note="LIPA16 repeat: matches 5509. .6157 of consensus
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e="MIX repeat: matches 48. .146 of consensus"
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4. .29607
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                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                              /note="AluSx repeat: matches 1. .302 of consensus"
complement (57062. .57330)
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55455. .55553
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51005. .51316
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51887..52533
/note="12 repeat: matches 1434..2116 of consensus"
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6033, .56348
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55720. .56032
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                                                                                                                                                                                                                                                                                     Secreted protein; cancer; tumour; neurodegenerative disorder; developmental abnormality; foetal deficiency; blood disorder; CNS disorder; inmune system disease; allergy; blood disease; hepatic disease; renal disease; diabetes; inflammation; allergy; ischemic shock; Alzheimer's; cognitive disorder; schizophrenia; cardiovascular disorder; prostate disease; asthma; osteoporosis; arthritis; ss.
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                                                                                                                                                                                                                                                                                                                                                        DNA encoding a human secreted protein.
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19-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      secreted polypeptides in a sample or by determining the presence of mutations in the polynucleotides. Specific uses are described for each of the products, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, CNS disorders, disease of the immune system, autoimmune diseases, hepatic and renal disease, diabetes, inflammation, allergies, ischemic shock, Alzheimer's and cognitive disorders, schizophrenia, cardiovascular disorders, prostate diseases, asthma, disorders involving osteoclasts such as osteoporosis, arthritis or malignancies, diseases of testes, lung or thymus, dispestive/endocrine disorders, infections and AIDS. The polypeptides are also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 867 BP; 219 A; 231 C; 222 G; 192 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The specification describes secreted proteins and their corresponding polynucleotides which are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Pathological conditions can also be diagnosed by determining the amount of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated human genes encoding secreted polypeptides - useful diagnosis and treatment of pathalogical diseases.
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GCTTTGAAAAGGGGCAGAAGTATAGTGGGCGAGCTGCCCACCTGCTACAGTGAAGGGATCT
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                              AAGAATCAGCGAACAAAAGCCTCTAGGTCTTTCTTACCACAAACACCTCTCTGCCCACCT
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Pred. No. 5.4e-308;
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CA, Brewer LA,
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TGCTATGACCAATCTCGTGCCGAATTC 867
               TGCTATGACCAATCTCGTGCCGAATTC 867
                                                    GCCACTCGGATTTGAACCCCGGCTCCTCAAGGTCAGCTGTGTAGCCTTGANTGAAYCACC
                                                                                                                                   AAATCCGGGTATGCCGGGTGAGAATGAGCAGGACTAACACCTGGGTGTCATGGCAAGCCT
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Novel human secreted protein cDNA #2.
                                  04-DEC-2003
                                                                                           ADB47729
                                                                                           standard; cDNA;
                               (first entry)
                                                                                             867
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ss; gene; human; secreted protein; insulin; haemoglobin S; haemoglobin B; superoxidase; SOD; catalase; DNA repair protein; concogene; tumour suppressor; tumour necrosis factor; TNF; inflammation; blood vessel growth inhibition; immune response; immune system disorder; hyperproliferative disorder; neoplasm; cardiovascular disorder; peripheral artery disease; limb ischaemia; arterio-arterial fistula; arteriovenous fistula; congenital heart defect; neovascularisation disorder; wound healing; epithelial cell proliferation; neurological disease; Alzheimer's disease; epithelial cell proliferation; neurological disease; Alzheimer's disease; infectious disease. Parkinson's disease; Huntington's disease; mania; dementia;

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ADB47729
ADB
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05-AUG-1997;
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05-AUG-1997;
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97US-0054803P
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conservation of the training a mathiorating a machine of the condition. The conservation is useful for diagnosing a pathological condition or susceptibility to a pathological condition in a subject. The protein is condition in a subject of identifying a binding partner. The nucleic acid is useful for diagnosing pathological condition or a susceptibility to pathological condition or a susceptibility to pathological condition or a susceptibility to pathological condition in a subject. The protein is useful as reagents for differential identification of the tissues or cell types present in a condition or a susceptibility to pathological condition in a subject. The protein is useful as reagents for differential identification of the tissues or cell types present in a condition of the tissues or cell types present in a condition. The condition is condition of the tissues or cell types present in a condition of the tissues or cell types present in a condition of the tissues. The condition is condition in the condition of the activity of membrane bound receptor by competing consisting the activity of applypeptide e.g. an oncogene or tumour receptor, to reduce the activity of membrane bound receptor by competing consisting the activity of applypeptide e.g. by binding to a receptor, to reduce the activity of membrane bound receptor by competing consistent in the free ligand e.g. soluble tumour necrosis factor (NFP) consistent in the forter cell condition of the protein and the nucleic conditions to the response to proliferative cells or tissues. The protein and the nucleic condition in the protein and the nucleic conditions of other cell types where expression has been observed. The protein, the nucleic acid and antibodies are useful for treating, consensing diseases, disorders and/or conditions of cells as conditions of cells as conditions of cells are conditions of cells as conditions of cells are conditions of central cell proliferation, neurological diseases (such as Alzhaimer's disease, mania, dementia, etc. The pr
             04-AUG-1998;
04-FEB-1999;
06-OCT-2000;
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19-AUG-1997;
19-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human secreted proteins useful for treating and/or diagnosing disorders of immune system, cardiovascular disorders such as peripheral artery disease, neurological diseases such as Alzhelmer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GREE/)
(FERR/)
(YUGG/)
(NIJJ/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to novel human secreted proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 205; 333pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       artery disease, neurological diseases such as
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OLSEN H S.
YOUNG P B.
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FERRIE A M.
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BREWER LA.
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                TGCTATGACCAATCTCGTGCCGAATTC 867
                                                                     GCCACTCGGATTTGAACCCCGGCTCCTCAAGGTCAGCTGTGTAGCCCTTGANTGAAYCACC
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TGCTATGACCAATCTCGTGCCGAATTC 867
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Pred. No. 5.4e-308;
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Best Local Sim
Matches 823;
                                                                                                                                                                                                                                                                                                                                   (ant)agonists are useful in the diagnosis, treatment and prevention of:
(a) cancer, e.g. breast and ovarian cancer and other cancers of the
adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,
lung or urogenital; (b) immune disorders e.g. Addison's disease,
allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
arthritis and ulcerative colitis; (c) cardiovascular disorders such as
myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g.
cerebral anoxia and epilepsy, and (f) infectious diseases such as viral,
bacterial, fungal and parasitic infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; nootropic; neuroprotective; cytostatic; virucide; dermatological; immunosuppressive; antiinflammatory; anti-HIV; vulnerary; antibacterial; antiparkinsonian; antisickling; antianaemic; antiinflammatory; antiiheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiucer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; infection; vaccine; cardiovascular disorder; neurological disease; nephrotropic;
                                                                                                                                                                                                                                                                                                  Sequence 58181 BP; 15503 A; 12755 C; 13504 G; 16419 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel human genes (ABZ66891-ABZ68209) and the encoded secreted proteins (ABP99470-ABP99872) useful for preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 2272-2286; 2423pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human secreted proteins encoded by genes contained in cDNA clones (e.g. HGCAC19), useful for preventing, treating or diagnosing e.g. AID multiple sclerosis, herpes virus, leukemia, tick-borne encephalitis or
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12-SEP-2001; 2001US-00950082
12-SEP-2001; 2001US-00950083
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activity are useful for diagnosing of treating cancers or other hyperproliferative disorders. Additionally, the secreted proteins and their nucleic acids may also be used in the treatment of autoimmune disorders, inflammatory disorders, diseases involving angiogenesis, AIDS (acquired immunodeficiency syndrome), hepatitis, anaemia, and to promote wound healing. Nucleic acids of the invention may be used for chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     identification, chromosome mapping, in gene therapy, for identifying individuals from minute biological samples, as hybridisation probes, and as molecular weight markers. The present sequence represents a human secreted protein genomic fragment referred to in the disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human secreted proteins and nucleic acids, useful for detecting or treating cancer or other hyperproliferative disorders, autoimmune disorders, inflammatory disorders, HIV disease, hepatitis or anemia.
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                                                                                          New human secreted proteins and nucleic acid molecules, useful for preparing a diagnostic or pharmaceutical composition for diagnosing, preventing or treating hematopoietic or hematologic disorders, e.g.
                                                                                                                                                                                                                                                         27-MAR-2001; 2001US-0278650P.
12-SEP-2001; 2001US-00950082.
12-SEP-2001; 2001US-00950083.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       gastrointestinal disorder; duodenal ulcer; gastroenteritis; gene;
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infectious disease; HIV; AIDS; endocrine disorder; diabetes;
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                                                                               anemia or
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The invention comprises the amino acid and coding sequences of human secreted proteins. The DNA and protein sequences of the invention ar

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Best Local Sim
Matches 823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for detecting, preventing, diagnosing, prognosticating, treating or ameliorating: haematopoietic or haematological disorders (e.g. anaemia and haemophilia); inflammatory disorders (e.g. inflammatory bowel disease and Crohn's disease); neoplastic disease (e.g. cancer and leukaemia); wound healing and disorders of epithelial cell proliferation; immune disorders (e.g. autoimmune disorders and asthmatic disorders); cardiovascular disorders (e.g. atherosclerosis and myocarditis); infectious disease (e.g. HIVAIDS); endocrine disorders (e.g. diabetes); and gastroenteritis). The present DNA sequence was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 58181 BP; 15503 A; 12755 C; 13504 G; 16419 T; 0 U; 0 Other;
                                                                      51845
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                                784 ACTOGGATTTGAACCCCGGCTCCTCAAGGTCAGCTGTGTAGCCTTGA 830
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                                                                                        AGAGCAGAGGTGGGCAGGCCCTTTTGATTAATGTATCATTCTTGAATGCAAGCTTCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTCACCTGACATTTTGGGAACTCCCCCCCCACGGCCATAACTGATCTGCAGAGGTAAGACC
                                                                    TCCGGGTATGCCGGGTGAGAATGAGCAGGACTAACACCTGGGTGTCATGGCAAGCCTCCA
                                                                                                                                                                          TCCGGGTATGCCGGGTGAGAATGAGCAGGACTAACACCTGGGTGTCATGGCAAGCCTCCA
                                                                                                                                                                                                                AGAGCAGAGGTGGGCAGGCCCTTTTGATTAATGTATCATTCTTGAATGCAAGCTTCAAAA
                                                                                                                                                                                                                                                                                    GCCAAAGGACTCCGGAGGAGAGAGGCCCAATAAGGCTGGCGCTATTTCCGATCCATAGAG
                                                                                                                                                                                                                                                                                                                    GCCAAAGGACTCCGGAGGAGAGAGGCCCAATAAGGCTGGTGCTATTTCCGATCCATAGAG
                                                                                                                                                                                                                                                                                                                                                        ACCCCACGGGAGCCTTACACAAGTCCAAAACAGGCCCAAATGCATTCATGAGCAGGGGGAG
                                                                                                                                                                                                                                                                                                                                                                                          ACCCCACGGGAG - CTTACACAAGTYCAAACAGGCCCAAATGCATTCATGAGCAGGGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                            AAATACTCACACTITGAGGTGCTCGCCCTCTTCATCAGCCAGCTCTAACTTAAGCCAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAAGGGGCAGAAGTATAGTGGGCGAGGCTGCCCACCTGCTACAGTGAAGGGATCTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAAGGGGCAGAAGTATAGTGGGCGA-GCTGCCCACCTGCTACAGTGAAGGGATCTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCAGCGAACAAAAGCCTCTAGGTCTTTCTTACCACAAACACCTCTCTGCCCACCTGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCAGCGAACAAAGCCTCTAGGTCTTTCTTACCACAAACACCTCTCTGCCCCACCTGCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGAGCCACTGCGCCCAGCCGGTCTTTTTAAACATTCCCCCAGGACTGTACAGCCCAACCCCAT 52386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGAGCCACTGCGCCCAGCCGGTCTTTTTAAACATTCCCCCAGGACTGTACAGCCAACCCAT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGAACTCCTGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGAACTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITTITTTTTTTTTTTTTAAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATGGTCT
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99.5%;
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Pred. No. 7.
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7.9e-168;
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   51739
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26-SEP-2000;
27-SEP-2000;
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25-SEP-2000;
25-SEP-2000;
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25-SEP-2000;
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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic; gene therapy; antineoplastic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prostate cancer related gene sequence SEQ ID NO:7550
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22-SEP-2000;
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20-SEP-2000;
                                                                                                                                                       2000US-0209473P.
2000US-0209473P.
2000US-0233133P.
2000US-0234039P.
2000US-0234052P.
2000US-02349549.
2000US-02349549.
2000US-0235082P.
2000US-0235637P.
2000US-0235637P.
2000US-0235637P.
2000US-0235637P.
2000US-0235711P.
2000US-0235840P.
2000US-0235840P.
2000US-0235840P.
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2000US-0235840P.
2000US-0235840P.
2000US-023603P.
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2000US-023603P.
2000US-023603P.
2000US-0237173P.
2000US-0237173P.
2000US-0237294P.
2000US-0237294P.
2000US-0237604P.
2000US-0237604P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               carcinoma; antitumour; cancerous;
lastic; Wilm's tumour; adenocarcinoma;
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Young PE, Soppet DR,

Augustus Weaver Z

Carter KC,

Ebner 'n,

Endress

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Horrigan

(AVAL-) AVALON PHARM.

WPI; 2002-188264/24.

Claim 1; SEQ ID NO 7550; 44pp; English.

expression of a gene of a signature gene set.

Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change

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HARRA BARA KANANA KANAN
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      18-SEP-2000;
18-SEP-2000;
20-SEP-2000;
20-SEP-2000;
20-SEP-2000;
22-SEP-2000;
22-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
                                                                                                                                                                                                                                     05-JUN-2000;
                                                                                                                                                                                                                                                                                                                                   30-MAY-2001; 2001WO-US010838.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200194629-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lung cancer related gene sequence SEQ ID NO:5143.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 145831 BP; 37379 A; 35440 C; 35158 G; 37854 T; 0 U; 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a method (M1) for screening for an neoplastic agent. The method involves exposing cells to a chemical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGC 124
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; 2000US-0209473P.

2000US-0239531P.

2000US-0233133P.

2000US-0233677P.

2000US-0234009P.

2000US-0234034P.

2000US-0234054P.

2000US-0234509P.

2000US-0234507P.
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25-SEP-2000;
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25-SEP-2000;
25-SEP-2000;
25-SEP-2000;
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2000US-0234924P.
2000US-0235077P.
2000US-0235082P.
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2000US-0245084P
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2000US-0237425P
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2000US-0236891P.
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t DR, Augustus Weaver Z 3 Carter KC, Ebner R, Endress

Screening for anti-neoplastic agent involves exposing agent to be tested for anti-neoplastic activity, and cin expression of a gene of a signature gene set. osing cells to a chemical and determining a change

Claim 1; SEQ ID NO 5143; 44pp; English.

The present invention describes a method (M1) for screening for an anticc neoplastic agent. The method involves exposing cells to a chemical agent
to be tested for anti-neoplastic activity, determining a change in
cc expression of at least one gene (I) of a signature gene set, where (I)
cc expression is indicative of anti-neoplastic activity. (I) has cytostatic
expression is indicative of anti-neoplastic activity. (I) has cytostatic
activity and can be used in gene therapy. M1 can be used for screening an
anti-neoplastic agent, and can be used for producing a product which is
the data collected with respect to the anti-neoplastic agent as a result
of M1, and the data is sufficient to convey the chemical structure and/or
properties of the agent. M1 can be used in the treatment of cancer such
as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
cancer, infiltrating ductal cancer, infiltrating lobilar cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's

Sequence 145831 BP; 37379 A; 35440 C; 35158 G; 37854 T; 0 U; 0 Other;

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Matches
                                                      Local Similarity
27 AGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATGGTCTCGAACTCCTGACCTCGTGATC
                                       98;
                                       Conservative
                                                      11.3%; Score 98; DB 6; 100.0%; Pred. No. 5.1e-27
                                         0; Mismatches
                                                                 Length 145831;
                                         Indels
                                         0
                                      Gaps
                 86
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Horrigan

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RESULT 8
ABL68588/c
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                      25-SEP-2000; 2000US-0235082P-25-SEP-2000; 2000US-023538P-25-2000; 2000US-0235280P-26-SEP-2000; 2000US-023538P-26-SEP-2000; 2000US-023563P-26-SEP-2000; 2000US-023571P-26-SEP-2000; 2000US-0235720P-27-SEP-2000; 2000US-0235840P-27-SEP-2000; 2000US-023583P-26-SEP-2000; 2000US-0235032P-28-SEP-2000; 2000US-0236032P-28-SEP-2000; 2000US-0236034P-28-SEP-2000; 2000US-023611P-28-SEP-2000; 2000US-023611P-28-SEP-2000; 2000US-023611P-28-SEP-2000; 2000US-023611P-29-SEP-2000; 2000US-023611P-29-SEP-2000; 2000US-023611P-29-SEP-2000; 2000US-023691P-02-CCT-2000; 2000US-0237172P-29-SEP-2000; 2000US-0237173P-02-CCT-2000; 2000US-0237173P-02-CCT-2000; 2000US-0237173P-02-CCT-2000; 2000US-02371425P-03-CCT-2000; 2000US-0237459P-03-CCT-2000; 2000US-0237604P-03-CCT-2000; 2000US-0237604P-03-CCT-2000; 2000US-0237604P-01-NOV-2000; 2000US-0237604P-01-NOV-2000; 2000US-0237604P-01-NOV-2000; 2000US-0237604P-01-NOV-2000; 2000US-0237604P-01-NOV-2000; 2000US-0237604P-01-NOV-2000; 2000US-0237604P-01-NOV-2000; 2000US-0244867P-01-NOV-2000; 2000US-0245084P-01-NOV-2000; 2000US-0245084P-01
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22-SEP-2000;
22-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; ca
stomach;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-SEP-2000;
25-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2001; 2001WO-US010838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              stomach; lung; prostate; pancreas; cytostatic; gene therapy; antineop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL68588 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kidney cancer related gene sequence
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2000US-0235077P.
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prostate; pancreas; carcinoma; antitumour; cancero
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a method (M1) for screening for an anti-
CC neeplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL6164
CC comprises a sequence (S) selected from 8447 sequences (given in ABL6164
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. MI can be used for screening an
CC activity and can be used in gene therapy. MI can be used for screening an
CC the data collected with respect to the anti-neoplastic agent as a result
CC of MI, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. MI can be used in the treatment of cancer such
CC prostate or pancreatic cancer, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC ell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
  05-JUN-2000; 2000US-0209473P
05-JUN-2000; 2000US-0209531P:
18-SEP-2000; 2000US-0233138P
18-SEP-2000; 2000US-0233617P
                                                                                                                                                                                                                                                                                                                                                                        cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human;
                                                                                                                                      30-MAY-2001;
                                                                                                                                                                                         13-DEC-2001.
                                                                                                                                                                                                                                          MO200194629-A2
                                                                                                                                                                                                                                                                                                                                                                                                    stomach;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Colon adenocarcinoma related gene sequence SEQ ID NO:646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL62309;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 145831 BP; 37379 A; 35440 C; 35158 G; 37854 T; 0 U; 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Young PE,
Soppet DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-188264/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38540
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                                                                                                                                                                                                                                                                                             eapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                           cancer; colon; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGC 124
                                                                                                                                                                                                                                                                                                                                                                                                       tung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGC
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Weaver Z;
                                                                                                                                                                                                                                                                                                                                                                  er; colon; breast; ovary; oesophagus; kidney; thyroid;
ng; prostate; pancreas; carcinoma; antitumour; cancerous;
gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                      2001WO-US010838.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carter
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5.1e-27
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Length 145831; Indels

Other;

<u>.</u>,

Gaps

98 0;

Ś 문

87

CGCCCGCCTCGGCCTCCCAAAGTGCTGCGATTACAGGC 124

Matches

98;

Conservative

0

100.0%;

Pred No. 5.1e-27; Mismatches

Indels

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Gaps

0

8 38541

Best Local Similarity

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26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
27-SEP-2000;
27-SEP-2000;
28-SEP-2000;
28-SEP-2000;
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25-SEP-2000;
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2000US-0234034P.
2000US-0234052P.
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(AVAL-) AVALON PHARM

Carter గ్గ Ebner R,

2002-188264/24.

Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.

Claim 1; SEQ ID NO 646; 44pp; English.

The present invention describes a method (MI) for screening for an anticone complastic agent. The method involves exposing cells to a chemical agent
cone tested for anti-neoplastic activity, determining a change in
comprises a sequence (S) selected from 847 sequences (given in ABL6164
comprises a sequence (S) selected from 847 sequences (given in ABL6164
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comprises a sequence (S) selected from 847 sequences (given in ABL6164
comprises a sequence (S) selected from 847 sequences (given in ABL6164
concervity and can be used in can be used for screening an anti-neoplastic agent, and can be used for producing a product which is
the data collected with respect to the anti-neoplastic agent as a result
of M1, and the data is sufficient to convey the chemical structure and/or
properties of the agent. MI can be used in the treatment of cancer such
as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
prostate or pancreatic cancer, infiltrating lobular cancer, squamous
cell carcer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's

Sequence 145831 BP; 37379 A; 35440 C; 35158 G; 37854 T; 0 U; 0 Other;

Score 98;

DB 6;

Query Match

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KARABARRASKEKERKEKKEKKEKERKARASSOSOSOSOSOSOSOS
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                                                       The present invention relates to methods of diagnosing breast cancer in a patient, which comprise detecting the level of expression in a tissue sample of two or more genes selected from those shown in ABT09867-ABT11112, where a differential expression of the genes indicates breast cancer. The methods are useful in diagnosing, treating, detecting the progression, and in monitoring treatment of breast cancer in patients. The methods are also useful as a screening tool for agents that modulate the onset or progression of breast cancer. The breast cancer genes may be used as diagnostic markers for the prediction or identification of the malignant state of breast tissue, for confirming the type and progression of cancer, and for drug screening and assays. The present sequence is a coding sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in the patient of the printed specification, but was obtained in the patient of the printed specification.
Sequence 145831 BP; 37379 A; 35440 C; 35158 G; 37854 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Diagnosing breast cancer in a patient comprises detecting the level gene expression in cell or tissue samples, where a differential gene expression is indicative of breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 283; 260pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-2001; 2001US-0263757P
25-APR-2001; 2001US-0286090P
23-MAY-2001; 2001US-0292517P
                                       ftp.wipo.int/pub.published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human breast cancer associated coding sequence SEQ ID NO: 283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JAN-2002; 2002WO-US002176.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; breast specific gene; breast cancer; differential expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABT10149 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENE-) GENE LOGIC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38540 CGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGC 38503
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Query Match Best Local &

Local Similarity

11.3%; Score 98; DB 6; ilarity 100.0%; Pred. No. 5.1e-2 Conservative 0; Mismatches

5.1e-27;

Length 145831; Indels

0

Gaps

98

22-A 23-A 30-A 01-S 01-S 01-S 05-S 06-S 06-S						XXXXXXX	Db Oy Db
22-AUG-2000; 2000US-02218268 23-AUG-2000; 2000US-0227182P 23-AUG-2000; 2000US-0227182P 30-AUG-2000; 2000US-022909P 01-SEP-2000; 2000US-0229343P 01-SEP-2000; 2000US-0229344P 01-SEP-2000; 2000US-0229345P 01-SEP-2000; 2000US-0229345P 05-SEP-2000; 2000US-0229345P 06-SEP-2000; 2000US-0229345P 06-SEP-2000; 2000US-0239345P 06-SEP-2000; 2000US-0239343P 06-SEP-2000; 2000US-0239343P 06-SEP-2000; 2000US-0230433P		14-JUL-2000; 2000US-0218290P. 26-JUL-2000; 2000US-0220963P. 26-JUL-2000; 2000US-0220964P. 14-AUG-2000; 2000US-0224518P. 14-AUG-2000; 2000US-0224519P. 14-AUG-2000; 2000US-0225213P. 14-AUG-2000; 2000US-0225214P. 14-AUG-2000; 2000US-0225266P. 14-AUG-2000; 2000US-0225266P.	18-APR-2000; 2000US-0198123P. 19-WAY-2000; 2000US-0205515P. 07-JUN-2000; 2000US-0209467P. 28-JUN-2000; 2000US-0214886P. 30-JUN-2000; 2000US-0215135P. 07-JUL-2000; 2000US-0215647P. 07-JUL-2000; 2000US-0215680P. 11-JUL-2000; 2000US-0217487P. 11-JUL-2000; 2000US-0217487P.		Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds. Homo sapiens. W0200157182-A2.	AAK82012; 07-NOV-2001 (first entry) Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36824.	Db 38600 AGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATGGTCTCGAACTCCTGACCTCGTGATC 38541 Qy 87 CGCCGGCCTCGGGCCTCCCAAAGTGCTGGGATTACAGGC 124
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17.NOV-2	08-NOV-2000; 2000US-02465 08-NOV-2000; 2000US-02465 08-NOV-2000; 2000US-02465 08-NOV-2000; 2000US-02466 08-NOV-2000; 2000US-02466 08-NOV-2000; 2000US-02466 08-NOV-2000; 2000US-02466 17-NOV-2000; 2000US-02492	08-NOV-2000; 2000US-02464 08-NOV-2000; 2000US-02464 08-NOV-2000; 2000US-02464 08-NOV-2000; 2000US-02464 08-NOV-2000; 2000US-02465 08-NOV-2000; 2000US-02465 08-NOV-2000; 2000US-02465 08-NOV-2000; 2000US-02465 08-NOV-2000; 2000US-02465	20-OCT-2000; 2000US-02405 20-OCT-2000; 2000US-02411 20-OCT-2000; 2000US-02411 20-OCT-2000; 2000US-02417 20-OCT-2000; 2000US-02417 20-OCT-2000; 2000US-02418 20-OCT-2000; 2000US-02418 20-OCT-2000; 2000US-02418 20-OCT-2000; 2000US-02418 01-NOV-2000; 2000US-02418	29-SEP-2000; 2000US-0236; 29-SEP-2000; 2000US-0236; 29-SEP-2000; 2000US-0236; 02-OCT-2000; 2000US-02370; 02-OCT-2000; 2000US-0239; 03-OCT-2000; 2000US-0239;	25-SEP-2000; 2000US-02345 25-SEP-2000; 2000US-02345 26-SEP-2000; 2000US-0235 27-SEP-2000; 2000US-0235 27-SEP-2000; 2000US-0235 27-SEP-2000; 2000US-0235 29-SEP-2000; 2000US-0235	14-SEP-2000; 2000US-0232 14-SEP-2000; 2000US-0232 14-SEP-2000; 2000US-0233 14-SEP-2000; 2000US-0233 14-SEP-2000; 2000US-0233 14-SEP-2000; 2000US-0234 21-SEP-2000; 2000US-0234 21-SEP-2000; 2000US-0234	08-SEP-2000; 2000US-02311 08-SEP-2000; 2000US-02311 08-SEP-2000; 2000US-02314 08-SEP-2000; 2000US-02314 08-SEP-2000; 2000US-02320 08-SEP-2000; 2000US-02320 12-SEP-2000; 2000US-02321 14-SEP-2000; 2000US-02321 14-SEP-2000; 2000US-02321 14-SEP-2000; 2000US-02323

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                                                                                                                                                                                                                                                                                                                                                                                             CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM62170 to AAM91921. (I) have cytostatic cc activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) inserting the CC polynucleotides may be used to produce the secreted (I), by inserting the CC polynucleotides may be used to produce the secreted (I), by inserting the CC protein. (I) proteins and polynucleotides may be used to prevent, CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic antigen genomic CC sequences from the present invention. AAK5492 to AAK5950 and AAM82169 CC represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                             Matches
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Best Local
             Human genemic DNA SEQ ID NO 196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                          AA162868;
                                                                                                       AAI62868 standard; DNA;
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17-NOV-2000;
17-NOV-2000;
                                            22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                         Sequence 49561 BP; 14811 A; 9800 C; 9812 G; 15138 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 36824; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding human immune/hematopoietic antigen polypeptides
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                                                                                                                                                                                                  96 CGGCCTCCCAAAGTGCTGGGATTACA 121
                                                                                                                                                                                                                                                                  36 GGGGTTTCACCGTGTTAGCCAGGATGGTCTCGAACTCCTGACCTCGTGATCCGCCCCGCCT 95
                                                                                                                                                                                                                                                                                                             86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tor preventing,
                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                   CGGCCTCCCAAAGTGCTGGGATTACA 13212
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                                                                                                                                                                                                                                                                                                           Conservative
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2000US-0249265P.
2000US-0249299P.
2000US-0249299P.
2000US-0250160P.
2000US-0250160P.
2000US-0251030P.
2000US-0251989P.
2000US-0251989P.
2000US-0251869P.
2000US-0251868P.
                                           (first entry)
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2000US-0251990P.
2000US-0254097P.
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Pred. No. 1.6e-
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The invention relates to novel genes (AAI62752-AAI62961) and proteins (AAM4247-AAM42415) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular discorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic

Novel plasma membrane associated proteins useful for diagnosing, treating, preventing and/or prognosing disorders related to the including cancer, immune response and neuronal disorders.

proteins,

WPI; 2001-476225/51.

Barash SC,

Ruben SM;

Example 2; SEQ ID NO 196; 532pp + Sequence Listing; English.

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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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08-NOV-2000;
17-NOV-2000;
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13-OCT-2000;
08-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianeemic; antiarthritic; cancer; antitheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiucer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; antiparasitic; cardiant; immune disorder; cardiovascular disorder;
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19-MAY-2000;
                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurological disease; infection; nephrotropic; gene therapy; vaccine;
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2000US-0236367P.
2000US-0239937P.
2000US-0246476P.
2000US-0246477P.
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2000US-0249214P-
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2000US-0246528P.
2000US-0249210P.
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2000US-0230437P.
2000US-0231243P.
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2000US-0251990P
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2000US-0256719P.
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RESULT 13
AAH09234
ID AAH09
XX AH09
DT 26-JU
XX Human
XX Homo
XX Homo
XX Homo
XX 29-JU
PR 29-JU
PR 29-JU
PR 29-JU
PR 11-JI
PR 11-
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Best Local :
                     length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the comprising a sequence comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 5'-end sequence which comprises and the comprise oligonucleotide which comprises as 1-end sequence, where the oligonucleotide which comprises as 1-end sequence, where the oligonucleotide comprises as 1-end sequence those defined in the specification. The primer sets can be used in antisence therapy and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
   gene therapy. The primers are useful for synthesising polynucleotides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-FEB-2001.
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the printed
                                                                                                                                                                                                                                                                                                                                                                 The present invention describes primer sets for synthesising 5602 full-
                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; SEQ ID NO 6069; 2537pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cDNA clone (3'-primer)
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27-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCCTGACCTCGTGATCCGCCCGCCCTCGGCCTCCCAAAGTGCTGGGGATTACAGGCATGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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2000JP-00183767.
2000JP-00241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO:6069.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashi K,
ı A, Nagai K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saito K,
(, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 267
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Best Local S
Matches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-00-1999; 99UP-000-1
27-AUG-1999; 99UP-00118776.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cDNA sequence SEQ ID NO:13457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 579 BP; 139 A; 141 C; 114 G; 180 T; 0 U; 5 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-318749/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HELI-) HELIX RES INST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sugiyama
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nishikawa
T, Wakama
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Le
. 9.3e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Otsuki
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:
(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end

sequence

and an oligonucleotide comprising

complementary

ç

Primer sets for synthesizing polynucleotides, particularly the 5602 ful length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length

Claim 8;

SEQ ID NO 13457; 2537pp + Sequence Listing; English

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Best Local S
Matches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cONAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cONAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AH03166 to AAH13628 and AH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13639 to AAH13632 represent
                                                                                                      Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cDNA differentially expressed in granulocytic cells #133.
                                                                                                                                                                                    WPI; 2002-435328/46.
                                                                                                                                                                                                                      Beazer-Barclay Y, Weissman SM,
                                                                                                                                                                                                                                                                                                03-OCT-2000; 2000US-0237189P
                                                                                                                                                                                                                                                                                                                                    03-OCT-2001; 2001WO-US030821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome; inflammatory bowel dis Crohn's disease, ulcerative colitis; periodontal disease, granulocyte activation; chronic inflammation; allergy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK83562 standard; cDNA; 139904 BP
                                                                                                                                                                                                                                                                                                                                                                                                              WO200228999-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; ss; granulocytic cell; DNA chip; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1555 BP; 488 A; 296 C; 332 G; 439 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                            (GENE-) GENE LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1288 CAGGCATGAGCCAC 1275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1348 TGGTCTCGAACTCCTGACCTCGTGATCCGCCCCGCCTCGGCCTCCCAAAGTGCTGGGATTA 1289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.5%; Score 74;
100.0%; Pred. No.
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                                                                                                                                                                                                                      Yamaga S, Vockley 3;
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                                                                                                                                                                                                                                                                                                                                                                                           CC expression level to an expression level in an unactivated GC, where cdifferential expression of Gs is indicative of GCA. Also included are conditating (M2) GA by contacting GC with an agent that alters the CC expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a CC pathogen or sterile inflammatory disease using the gene expression cresponse in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of CC pathogen or sterile inflammatory disease, by detecting the level of CC pathogen or sterile inflammatory disease, by detecting the level of CC pathogen or sterile inflammatory disease, by detecting the level of CC pathogen or sterile inflammatory disease, by detecting the level of CC pathogen or sterile inflammatory disease, by detecting the level of configuration of the gene is indicative of inflammation; (4) treating CC (M5) an inflammation (especially chronic) or in a tissue, an allergic cresponse in a subject, exposure of a subject to a pathogen or sterile CC is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful CC is useful for detecting an agent capable of modulating GCA preferably in an CC (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation with an inflammatory disease (e.g. psocialsis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, capacitatory distress syndrome, inflammatory bowel disease, Croth's growth and the conditions. The present sequence for treating one of the above conditions. The present sequence represents a gene differentially exposure of a subject to a pathogen or sterile inflammatory bowel disease, croth's conditions. The present sequence represents a gene differentially exposure of the pathogen of the spatent did electronic format directly from WIPO at the proposal infection in the proposal conditions and the printed specification, but was obt
                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                       Sequence 139904 BP; 39268 A; 29759 C; 30173 G; 40704 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                               Local
26760 CAGGCATGAGCCAC 26747
                                                                                                        26820
                                                 120 CAGGCATGAGCCAC 133
                                                                                                                                                             60
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                                                                                                      TGGTCTCGAACTCCTGACCTCGTGATCCGCCCCGCCTCCGCCTCCCAAAGTGCTGGGATTA 26761
                                                                                                                                                             TGGTCTCGAACTCCTGACCTCGTGATCCGCCCCGCCTCGGCCTCCCAAAGTGCTGGGATTA 119
                                                                                                                                                                                                                 Conservative
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Job time : 337 secs Search completed: May 24, 2004, 16:57:18

The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA chip analysis as given in the specification, and comparing the

SEQ ID NO 133; 114pp; English.

V.

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Gapop 60.0 , Gapext 60.0
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867
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Copyright (c) 1993 - 2004 Compugen Ltd.
              /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US103_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US103_PUBCOMB.seq:*
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_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

C 14	c 12	c 11	c 10	9	B		6		0	Ų	2	ь	Result No.
70	70	70	71	75	75	98	98	98	98	867	867	867	Score
8.1	8.1	8.1	8.2	8.7	8.7	11.3	11.3	₽1. 3	11.3	100.0	100.0	100.0	Query
65454	548	548	269	267	267	145831		145831	145831	867	867	867	Query Match Length DB
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US-10-08/-192-190 US-10-293-864-11	US-10-027-632-249911	US-10-027-632-249911	US-09-867-701-10441	US-10-227-646-196	US-09-860-670-196	US-10-240-425-363	US-09-873-367C-646	US-09-954-456-2116	US-09-969-708-79	US-10-621-363-12	US-09-969-730-12	US-09-774-639-61	ID
Sequence 190, App Sequence 11, Appl		Sequence 249911,	Sequence 10441, A	Sequence 196, App	Sequence 196, App	Sequence 363, App	Sequence 646, App	Sequence 2116, Ap	Sequence 79, Appl	Sequence 12, Appl	Sequence 12, Appl	Sequence 61, Appl	Description

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Sequence 1456, Ap	Sequence 1455, Ap		1455	145.	Sequence 1453, Ap	1454	1453	868		173	e 397	397,	Sequence 114299,		Sequence 114299,	114298	Sequence 2336, Ap	Sequence 3, Appli	Œ	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Seguence 324711,			Sequence 324711,	Φ	Sequence 324709,	13366,	Sequence 13366, A

ALIGNMENTS

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US-09-774-639-61
US-09-774-639-61
Sequence 61, Application US/09774639
Publication No. US20030003555A1
GENERAL INFORMATION:
APPLICANT: ROSEON et al.
FITTLE OF INVENTION: 90 Human Secreted Proteins
FILE REFREENCE: PZ013P1
CURRENT APPLICATION UNMBER: US/09/774,639
CURRENT PAPLICATION NUMBER: US/09/774,639
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
PRIOR TILING DATE: EARLIER FILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 371
                                                                                                                                                                                                                                                                                                                             US-09-774-639-61
                                                                                                                                                                                                                          Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 867; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: P
                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SITE
LOCATION: (831)
OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGIH: 867
121 AGGCATGAGCCACTGCGCCCAGCCGGTCTTTTTAAACATTCCCCAGGACTGTACAGCCAA 180
                                             61
                                                                      61 GGTCTCGAACTCCTGAACCTCGTGATCCGCCCTCGGCCTCCCAAAGTGCTGGGATTAC 120
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                                                                                                                                                                   TCGAGTETTTTTTTTTTTTTTTTAAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGAT 60
                                             GGTCTCGAACTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTAC
                                                                                                                                       TCGAGTTTTTTTTTTTTTTTTTTTAAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGAT 60
                                                                                                                                                                                                                             100.0%; Score 867; D
100.0%; Pred. No. 0;
tive 0; Mismatches
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Sequence 12, Application US/09969730
Publication No. US2030054443A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 90 Human Secreted Proteins FILLR EREPERSUCE: P2013P2
CURRENT APPLICATION NUMBER: US/09/969,730
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 09/774,639
PRIOR APPLICATION NUMBER: 09/738,291
PRIOR APPLICATION NUMBER: 09/238,291
PRIOR APPLICATION NUMBER: 09/244,112
PRIOR APPLICATION NUMBER: 09/244,112
PRIOR APPLICATION NUMBER: 09/244,112
PRIOR APPLICATION NUMBER: 09/056,371
PRIOR APPLICATION NUMBER: 60/056,371
PRIOR APPLICATION NUMBER: 60/056,371
PRIOR APPLICATION NUMBER: 60/056,371
PRIOR APPLICATION NUMBER: 60/056,371
PRIOR APPLICATION NUMBER: 60/056,732
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US-09-969-730-12
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SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 12
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PRIOR FILING DATE: 1997-08-05
NUMBER OF SEQ ID NOS: 373
                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 867
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
FEATURE:
NAME/KEY: SITE
LOCATION: (831)
OTHER INFORMATION: n equals a,t,g, or
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OR APPLICATION NUMBER: 60/055,309
OR APPLICATION NUMBER: 60/055,319
OR APPLICATION NUMBER: 60/055,312
OR FILING DATE: 1997-08-05
OR APPLICATION NUMBER: 60/054,807
OR APPLICATION NUMBER: 60/054,807
OR FILING DATE: 1997-08-05
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OR APPLICATION NUMBER: 60/056,366
OR FILING DATE: 1997-08-19
OR APPLICATION NUMBER: 60/056,364
OR FILING DATE: 1997-08-19
OR APPLICATION NUMBER: 60/056,370
OR FILING DATE: 1997-08-19
OR APPLICATION NUMBER: 60/056,367
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FILING DATE: 1997-08-05
APPLICATION NUMBER: 60/055,310
FILING DATE: 1997-08-05
APPLICATION NUMBER: 60/054,798
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APPLICATION NUMBER: 60/056,557
FILING DATE: 1997-08-19
APPLICATION NUMBER: 60/056,563
FILING DATE: 1997-08-19
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APPLICATION NUMBER: 60/054,809
FILING DATE: 1997-08-05
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FILING DATE: 1997-08-05
APPLICATION NUMBER: 60/054,804
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APPLICATION NUMBER: 60/054,808
FILING DATE: 1997-08-05
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FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/055,311
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APPLICATION NUMBER: 60/056,365
FILING DATE: 1997-08-19
121 AGGCATGAGCCACTGCGCCCAGCCGGTCTTTTTAAACATTCCCCAGGACTGTACAGCCAA
                                                                                                                                                                                                                      1 TCGAGTTTTTTTTTTTTTTTTTTAAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGAT
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                                                                     GGTCTCGAACTCCTGACCTCGTGATCCGCCCCGCCTCGGCCTCCCAAAGTGCTGGGATTAC
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RESULT 3
US-10-621-363-12
  PRIOR APPLICATION NUMBER: 09/965,730
PRIOR FILING DATE: 2001-10-06
PRIOR PPLICATION NUMBER: 09/774,639
PRIOR PILING DATE: 2001-02-01
PRIOR PELING DATE: 2000-10-06
PRIOR PELING DATE: 2000-10-06
PRIOR PPLICATION NUMBER: 09/234,291
PRIOR PPLICATION NUMBER: 09/244,112
PRIOR PILING DATE: 1999-02-04
PRIOR PPLICATION NUMBER: PCT/US98/16235
PRIOR PILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/056,371
PRIOR APPLICATION NUMBER: 60/056,371
PRIOR APPLICATION NUMBER: 60/056,732
PRIOR APPLICATION NUMBER: 60/056,732
PRIOR APPLICATION NUMBER: 60/056,732
PRIOR PILING DATE: 1997-08-19
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/106
Publication No. US20040023283A1
GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/621,363
CURRENT FILING DATE: 2003-07-18
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TITLE OF INVENTION: 90 Human Secreted Proteins
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Best Local .
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PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,364
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,370
PRIOR FILING DATE: 1997-08-19
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TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: misc feature
LOCATION: (831)
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                      721 ССАGGGCCGAСTGGCCAGAGACAGATCCGCAAGAGGCTCTGCAGCCAGCTCTGGTGCCAA
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                                                                                                         AAATCCGGGTATGCCGGGTGAGAATGAGCAGGACTAACACCTGGGTGTCATGGCAAGCCT 720
                                                                                                                                                                              GAGAGAGCAGAGGTGGGCAGGCCCTTTTGATTAATGTATCATTCTTGAATGCAAGCTTCA
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                                                                  AAATCCGGGTATGCCGGGTGAGAATGAGCAGGACTAACACCTGGGTGTCATGGCAAGCCT
                                                                                                                                                     GAGAGAGCAGAGGTGGGCAGGCCCTTTTGATTAATGTATCATTCTTGAATGCAAGCTTCA
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Conservative
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Pred. No. 0;
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US-09-969-708-79/c
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GENERAL INFORMATION:
APPLICANT: Augustus, Meena
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
TITLE OF INVENTION: Sets
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Best Local (
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                                                               TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer TITLE OF INVENTION: Sees
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR PRIOR PRIOR DATE: 2000-09-25
PRIOR PRIOR PRIOR DATE: 2000-09-26
PRIOR PRIOR DATE: 2000-09-26
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CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: US/60/237,606
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,608
PRIOR APPLICATION NUMBER: US/60/237,608
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,425
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NUMBER OF SEQ ID NOS: 658
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FILING DATE: 2000-09-26
APPLICATION NUMBER: US/60/235,711
                                                APPLICATION NUMBER: US/60/235,638
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100.0%; Pred. No. 5.2e-40;
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PRIOR APPLICATION NUMBER: U.S. 60/236,842
PRIOR APPLICATION NUMBER: U.S. 60/244,867
PRIOR APPLICATION NUMBER: U.S. 60/244,867
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: U.S. 60/245,084
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 1067
SOPTMARE: PAtentin version 3.0
SEQ ID NO 646
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US-09-873-367C-646/c
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-2116
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Best Local Similarity
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TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
TITLE OF INVENTION: Signature Gene Sets
FILE REFERENCE: 689290-64
CURRENT APPLICATION NUMBER: US/09/873,367C
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: U.S. 60/236,891
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PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
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PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
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ORGANISM: Homo sapiens
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Endress, Gregory
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100.0%; Pred. No. 5.2e-40
tive 0; Mismatches 0;
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SEQ ID NO 363
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                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/860,670 CURRENT FILING DATE: 2001-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ruben et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA127P1
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CURRENT APPLICATION NUMBER: US/10/240,425
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: PCT/US01/09847
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 60/193,446
PRIOR APPLICATION NUMBER: US 60/193,446
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 1588
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APPLICANT: Wetzel, Jon C.
APPLICANT: Wetzel, Uwe
APPLICANT: Vockley, Joseph G.
TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
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                                                                                                                                                                                                                                                                          LENGTH: 267
TYPE: DNA
ORGANISM: Homo sapiens
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Local Similarity 100.0%;
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253 CCACTGCGCCCAGCC 267
                      130 CCACTGCGCCCAGCC 144
                                                                                   193 CTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAG 252
                                                                                                              70 CTCCTGACCTCGTGATCCGCCCGCCCTCGGCCTCCCAAAGTGCTGGGGATTACAGGCATGAG 129
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                                                                                                                                                                                    h 8.7%; Score 75; DB 9; Similarity 100.0%; Pred. No. 5.3e-2
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                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US20040033502A1
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                                                                                                                                                                    0
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                                                                                                                                                                    Mismatches
                                                                                                                                                                                    5.3e-28;
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                                                                                                                                                                                                           Length 267;
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                                                                                                                                                                    Indels
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US-09-867-701-10441/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 196, Applic Publication No. US20 GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PastSEQ for Windows Version 4.0 SEQ ID NO 10441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 196
LENGTH: 267
                                                                                                                                                                       Matches
                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT PILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/227,646
CURRENT FILLING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: US/09/860,670
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ruben et al. TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PA127P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                           ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                         LENGTH: 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.0%;
103 TGCGCCCAGCC 93
                                           134 TGCGCCCAGCC 144
                                                                                  163 TGACCTCGTGATCCGCCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCAC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 CTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 CCACTGCGCCCAGCC 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 CCACTGCGCCCAGCC 144
                                                                                                                           74 TGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCAC 133
                                                                                                                                                                  71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 CTCCTGACCTCGTGATCCGCCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAG 129
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o. US20030235829A1
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                                                                                                                                                                                           100.0%;
                                                                                                                                                                  8.2%; Score 71; DB 9; Le
100.0%; Pred. No. 6e-26;
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100.0%; Pred. No. 5.3e-28;
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RESULT 11 US-10-027-632-249911/c

Sequence 249911, Application US/10027632 Publication No. US20020198371A1

GENERAL INFORMATION

TYPE: DNA

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                                                                                      FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR PRILING DATE: 2000-03-29
PRIOR PRILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-24
PRIOR PRILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PRILING DATE: 1999-11-23
PRIOR PRILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PRILING DATE: 1999-09-28
PRIOR PRILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
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NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 249911
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PRIOR PRICING DATE: 2000-04-20
PRIOR PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PRIOR DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 325720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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100.0%; Pred. No. 1.9e-25;
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US-10-293-864-11

PEATURE:

TYPE: DNA ORGANISM: H. sapiens

ENGTH: 65454

Query Match

8.1%;

Score 70;

DB 17;

Length 65454;

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                                                                                                                                                                                                                                                  RESULT 14
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                                      Sequence 11, Application US/10293864
Publication No. US2004009245A1
GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF HUNTINGTIN INTERACTING PROTEIN 1 EXPRESSION
FILE REFERENCE: RTS-0432
CURRENT APPLICATION NUMBER: US/10/293,864
CURRENT FILING DATE: 2002-11-11
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Publication No. US20020182586A1
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Best Local :
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER PILE REFERENCE: 529452000122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70; Conservative
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Similarity 100.0%; Pred. No. 1.4e-22
70; Conservative 0; Mismatches
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GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT REPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/198,483

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 1999-10-224

PRIOR APPLICATION NUMBER: US 60/185,358

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-29

NUMBER OF SEQ ID NOS: 325720

SEQ ID NO 13366

LENGTH: 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-13366
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nes 68; Conserv
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